score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query

Result Š. AY006113 Homo sapi AB059449 Unculture

K00307 Halobacteri K03199 Halobacteri AJ306918 Homo sapi

Description

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9, 2004, 01:42:24 ; Search time 799.247 Seconds (without alignments) 5206.064 Million cell updates/sec
                                                                                                                  1 gggagaggaagagggaug......cgauaguacuggauccccc
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                3470272 seqs, 21671516995 residues
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Maximum Match 100%
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                                   OM nucleic - nucleic search, using sw model
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AX638759 Sequence
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CAR144444 Sequence
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Z660309 H.sapiens C
AK134550 MIAF-2413-S PRI 04-JAN-2002 AR141690 Sequence AX638748 Sequence A11877 Nucleotide A11878 Nucleotide AX638759 Sequence AX638759 Sequence AX638759 Sequence AB059200 Sus scrof AU046875 Rattus no AR141703 Sequence AX638760 Sequence AX333319 Sequence XX01221 Thermoplasm Padilla,O., Pujana,M., Lopez,A., Arman,M., Vila,J., Gimferrer,I., Places,L., Vives,J., Estivill,X. and Lozano,F. Cloning of a new member of the SRCR-SF Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. AR141692 Sequence AX638750 Sequence AR141696 Sequence AX181678 Sequence I76096 Sequence 4 Sequence linear exon 7. DNA אם 138 bp DN Homo sapiens partial SRCRB-S4D gene, AJ306918 ALIGNMENTS AJ306918.1 GI:18073567 SRCRB-S4D gene; SRCRB-S4D protein. Homo sapiens (human) Homo sapiens HSA306918 HALTRMI HCMET AY006113 AB059449 AB059200 AU046875 AR141692 AK638750 AK638756 AR141694 AR141694 AK638755 AK638755 AK638751 AK638751 AK638751 AK638751 AK638751 AK638751 AK638753 AK7784444 AF7328875 AR141690 AX638748 A11877 A11878 AR141702 AX638759 HUMTGMIM AX333319 TATRNMET AX181678 I76096 AX638760 AR141703 124 100 138 171 171 171 171 171 78 78 78 191 91 91 129 129 DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 1 HSA306918/c ORGANISM REFERENCE AUTHORS TITLE LOCUS υ υ Pred. No. is the number of results predicted by chance to have a

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[Thesis (1981) University of Illinois, Urbana] Contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their entry 1315 in Nucleic Acids Res. 11, rl-r54 (1983).
                                                                                                                                                                                                                                 'note="codon recognized: AUG; Met-tRNA-i (NAR: 1315)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium salinarum
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 78)
Nicoghosian, K., Gu, X.R. and Cedergren, R.
Halobacterium cutirubrum tRNs sequences
FEBS Lett. 193, 255-260 (1985)
Data kindly reviewed (26-MAR-1986) by K. Nicoghosian.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCMET 78 bp DNA linear Halobacterium cutirubrum transfer RNA-Met (CAU).
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/mol_type="genomic DNA"
/db_xref="taxon:2242"
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                                                                                                                             /organism="Haloferax volcanii"
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/mod_base=mlf
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Halobacterium salinarum
                                                                                                                                              /moi_type="tRNA"
/db_xref="taxon:2246"
1. .78
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                                                                                   Location/Qualifiers
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13
                                                                                                                                                                                                              product="tRNA-Met"
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The archaebacterial tRNAs follow general tRNA patterns, but have certain characteristics so far not reported for other tRNAs: all have 'cm' at position 55; "all' at position 55; "all' at characteristics so far not reported for other tRNAs: all lo; "mif" at position 55; "all obsition 15. Only archaebacteria modify the residue at position 15. Only archaebacteria modify the residue at position 15. Only archaebacteria modify the residue at position 55. "chosphorylated the initiator tRNA is unique in that it has a 5'-phosphorylated
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                   2 (bases 1 to 138)
Dizano,F.

Dizano,F.

Direct Submission
Submitted (25-APR-2001) Lozano F., Hospital Clinic, Servei
d'Immunologia, Villarroel 170, Barcelona 08036, SPAIN
3' end of intron 6 from bp 1 to 31; 5' end of intron 7 from bp 109
to 138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural characterization of the transfer ribonucleic acids from Halobacterium volcanii and other archaebacteria Unpublished (1981)
2. (bases 1 to 78)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 GAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Original source text: Halobacterium volcanii, strain DS2 (NCMB
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Halobacteriaceae; Haloferax.
1 (bases 1 to 78)
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Halobacterium volcanii initiator Met-tRNA-i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.8%; Score 23.8; DB 9;
45.3%; Pred. No. 2.6e+03;
cive 9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                            /usedin=AJ306912:84d mRNA
/usedin=AJ306913:84d cds
                                                                                                                                                                                          1. .138
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transfer RNA, transfer RNA-Met.
Haloferax volcanii
Haloferax volcanii
                                                                                                                                                                                                                               /mol_type="genomic_DNI/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                               /map="7q11.22-23"
31. .108
                                                                                                                                                                                                                                                                                                                                           'gene="SRCRB-S4D"
                                                                                                                                                                                                                                                                                                                                                                                  /gene="SRCRB-S4D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K00307.1 GI:174729
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Matches 34; Conservative
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Unpublished
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Gaps

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Indels

Length 78;

BCT 11-JUN-2003

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BCT 25-APR-2001

ORIGIN

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AB059200 181 bp DNA linear STS 19-MAR-2002
Sus scrofa domestica genomic DNA, chromosome 7, 346D10R, sequence
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Submitted (06-APR-2001) Yoshiyuki Ueno, Kajima Technical Research
Institute, Bio-environment group; Tibitakyu, 2-19-1, Chofu-shi,
Tokyo 182-0036, Japan (E-mail:yoshi-uokatri.kajima.co.jp,
Tel:81-424-89-7066(ex.2945), Fax:81-424-89-2896)
On Apr 24, 2001 this sequence version replaced gi:13620946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa domestica
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                               Ueno,Y., Haruta,S., Ishii,M. and Igarashi,Y.
Changes in Product Formation and Bacterial Community on
Carbohydrate Fermentation by Anaerobic Microflora -Effects of
Dilution Rate in Continuous Flow Stirred Tank Reactor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (30-MAR-2001) Sachiko Kiuchi, National Institute of
Agrobiological Sciences, Genome Research Group; 2 Ikenodai,
Kukizaki-machi, Inashiki-gun, Ibaraki 305-0901, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kiuchi,S., Inage,Y., Hiraiwa,H., Uenishi,H. and Yasue,H. Assignment of 280 swine genomic inserts including 31 microsatellites from BAC clones to the swine RH map (IMpRH Mamm. Genome 13 (2), 80-88 (2002)
                                                                                                    linear BCT ?
partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="uncultured bacterium"
/mol_type="genomic DNA"
/db_xref="taxon:77133"
/dcone="B2 538-14(B14)"
/note="DGGE fragment of anaerobic microflora"
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50.0%; Pred. No. 6e+03;
iive 8; Mismatches 17; Indels
                                                                                           99 bp DNA
Uncultured bacterium gene for 16S rRNA, clone: B2 538-14 (B14).
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                                                                                                                                                                                                                                           uncultured bacterium
Bacteria; environmental samples.
1 (sites)
                                                                                                                                                                                     AB059449.2 GI:13785490
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AB059200
  10 AGCTGCTG 3
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                                                          RESULT 5
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                                                                                                                                                                                                                                                                                                                                     AY006113 91 bp mRNA linear PRI 26-SEP-2000
Homo sapiens clone pbvb203 T cell receptor beta chain mRNA, partial
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Direct Submission

Submitted (31-U01-2000) Department of Microbiology and Immunology,

Temple University School of Medicine, 3400 N. Broad Street,

Philadelphia, Pa 19140, USA

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rejection contain oligoclonal T cells: persistence of identical clonally expanded TCR transcripts from the early post-transplantation period (endomyocardial biopsies) to chronic rejection (coronary arteries)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 GGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="pbvb203"
/tiseue_type="peripheral blood mononuclear cells"
/rearranged
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Slachta, C.A., Jeevanandam, V., Goldman, B.I., Lin, W.L. and
Platsoucas, C.D.
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Slachta,C.A., Jeevanandam,V., Goldman,B., Lin,W.L. and
Platsoucas,C.D.
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/protein id="AAG15616.1"

/db_xref="G1:10304545"

/translation="DSSFYICSASFEREDTDTQYFGFGTRLTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 91;
                                                                                                      Length 78;
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                                                                                                                                                Indels
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                                                                                                                                                8;
                                                                                                                                                                                                             23 ATTCCGCCGGCTCATAACCCGGAGATCGGTAGTTC 58
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1 Similarity 45.6%; Pred. No. 4.4e+03;
31; Conservative 9; Mismatches 28;
                                                                                                                                                                                       50 AUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUAC 85
                                                                                                      Score 23.2; DB 1;
Pred. No. 4.4e+03;
7; Mismatches B;
                   /note="1-methylinosine"
/mod_base=mli
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AY006113.1 GI:10304544
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                                                                                                    Query Match
24.2%;
Best Local Similarity · 58.3%;
Matches 21; Conservative
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Best Local Similarity
Matches 31; Conserv
modified base
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Method and reagent for inhibiting the expression of disease related
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                                          1 GGGAGAGAAGAAGAGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCC
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Thompson, J.D.
RNA polymerase III-based expression of therapeutic RNAs Patent: 1046886-A 3 14-NOV-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.7%; Score 21.8; DB 6; Length 108; llarity 52.3%; Pred. No. 1.3e+04; Conservative 4; Mismatches 27; Indels
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      Indels
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        20;
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Pred. No. 1.3e+04;
4; Mismatches 27;
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E PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 5889 from Patent EP1260586.
      6; Mismatches
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/db_xref="taxon:32644"

    .108
/organism="unknown"
/mol_type="unassigned DNA"

                                                                                                                                                                        Sequence 3 from patent US 6146886. AR141692
                                                                                                                                                                                                                                    AR141692.1 GI:15101208
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Best Local Similarity 52.3%;
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        28; Conservative
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67 ACCCC 71
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                                                                                                                                                                                              /clone_lib="Swine genomic BAC library, National Institute of Agrobiological Resources, Ibaraki, Japan" /note="synonym:Sus scrofa domesticus"
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The large-scale mapping of rat microsatellite markers
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research
Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno,
Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan
(E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="liver"
/note="085b01F=s'-TCTCTCCCTCCCTCCT-3'
085b01R=s'-AGACTTTGTACACACACGCA-3'"
(E-mail:sachikok@affrc.go.jp, Tel:81-298-38-8664,
Fax:81-298-38-8674)
Location/Qualifiers
                                                                              organism="Sus scrofa domestica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Brown Norway"
                                                                                                /mol_type="genomic DNA"
/sub_species="domestica"
/db_xref="taxon:9825"
                                                                                                                                                                                                                                                          1. .181
/standard_name="346D10R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="hepatocyte"
/tissue type="liver"
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/clone="085b01"
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Location/Qualifiers
                                                                                                                                                                              'clone="346D10"
                                                                                                                                        /db_xref="taxo
/chromosome="7
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PAT 08-AUG-2001
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Thompson,J.D.
RNA polymerase III-based expression of therapeutic RNAs
Patent: US 6146886-A 9 14-MOV-2000;
Location/Qualifiers
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Patent: US 6146886-A 5 14-NOV-2000;
Location/Qualifiers
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Best Local Similarity 52.3%; Pred. No. 1.3e+04;
Matches 34; Conservative 4; Mismatches 27; Indels
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Sequence 5 from patent US 6146886.
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Sequence 9 from patent US 6146886.
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1 (bases 1 to 133)
Thompson, J.D.
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7 ACAGCAGAGTGGCGCAGCGGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAA 66
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1 (Description)
Thompson, J.D.
Thompson, J.D.
RNA polymerase III-based expression of therapeutic RNAs
Patent: US 6146886-A 7 14-NOV-2000;
Location/Qualifiers
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Best Local Similarity 52.3%; Pred. No. 1.3e+04;
Matches 34; Conservative 4; Mismatches 27; Indels
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RIBOZYME PHARMACEUTICALS, INC. (US)
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Sequence 5893 from Patent EP1260586.
AX638754
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 5895 from Patent EP1260586.
AX638756
                                 133 bp Ri
Sequence 5891 from Patent BP1260586.
AX638752
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Abn88528 Coagulati Abn88526 Coagulati Abn88529 Coagulati Abn88508 Coagulati Abn88490 Coagulati Coagulati Coagulati Coagulati Coaqulati Coagulat Coagulati Coagulati Coagulati Coagulati Coagulati Coaqulat Coagulat Coagulat: Coagulat Coagulat Coagulat ADDR 8506
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Abn88530 Coagulati Abn88559 Coagulati Abn88507 Coagulati	Abn88511 Coagulati Abn88511 Coagulati Abn88533 Coagulati Abn88492 Coaqulati		Abn88518 Coagulati Abn88523 Coagulati Abn88514 Coagulati	000	Abn88488 Coagulati Abn88516 Coagulati Abn88513 Coagulati	Abn88520 Coagulati Abn88524 Coagulati Abz21242 FIXa apta
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ALIGNMENTS

RNA aptamer; identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis; Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:3 BP. 26-SEP-2001; 2001WO-US030004 26-SEP-2000; 2000US-0235654P ABN88490 standard; RNA; 96 (first entry) Sullenger BA, Rusconi CP; bypass graft surgery; ss WPI; 2002-479560/51 (UYDU-) UNIV DUKE. WO200226932-A2. Homo sapiens. Synthetic. 19-AUG-2002 04-APR-2002. ABN88490; RESULT 1 ABN88490

E2F Novel RNA aptamers that selectively bind coagulation pathway factors, E2 family members, Ang1 or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.

Claim 13; Fig 1A; 216pp; English

The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoietin-1 (Angi) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 nM or less. (I) (II) and (III) have cardiant and cyrostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

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the biological activity of the coagulation pathway factor in the warm-blooded vertebrate is modulated. (I) are also useful for treating cardiovascular diseases in the mammal. (II) are useful for modulating ESF activity in a warm-blooded vertebrate. (II) are useful for modulating ESF activity in a warm-blooded vertebrate. (I) are potent cardiovasulants and significantly delay the clotting time of normal human blasma or the activity in a warm-blooded vertebrate. (I) are potent cardiovasulants and significantly delay the clotting time of normal human continual hyperplasia following bypass graft surgery. (II) are useful for modulating angiogenesis. The RNA aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research bind, and for isolating and purifying substances to which they specifically bind. And so as a separation reagent for retrieving the targets to which they bind, and as a separation reagent for retrieving the targets to which they they specifically bind. ABN88488 to ABN88713 and ABB881231 represent context.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGAGAGAGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAGAGAGAAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
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Matches 96; Conservative
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The present invention describes RNA aptamers (1,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)

family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Ang1 or Ang2 activity in a mammal. Novel RNA aptamers that selectively bind coagulation pathway factors,

с. С

Rusconi

Sullenger BA,

WPI; 2002-479560/51.

Claim 13; Fig 1B; 216pp; English.

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angiopoietin-1 (Angl) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family commender, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate is modulated. (II) are also useful for modulating E2F activity in a warm-blooded vertebrate. (II) are useful for modulating activity in a warm-blooded vertebrate. (II) are useful for modulating and anticoagulants and significantly delay the clotting time of normal human coagulants and significantly delay the clotting time of normal human cuseful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for intimal hyperplasia following bypass graft surgery. (III) are useful for cascarch and therapeutic context. The aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic cragents to detect the presence or absence of target substances to which they comind, and as a separation reagent for retrieving the targets to which they be bind, and as a separation reagent for retrieving the targets to which they specifically bind. AbN88488 to ABN88713 and ABB81231 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel RNA aptamers that selectively bind coagulation pathway factors, E?
family members, Angl or Ang2, useful for modulating coagulation pathway
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Pred. No. 7.4e-13;
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78.78;
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Best Local Similarity
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ABN88504
                   %XGGGGGGGGGGGGGGGGGGGGGG
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The present invention describes RNA aptamers (1,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) anagopoietin-1 (Angl) or Ang2, respectively, where (1), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 mM or less. (1), (II) and (III) have cardiant and cycestatic activities. (1) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (1) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate (i) are also useful for modulating activity of the mammal. (II) are useful for modulating a warm-blooded vertebrate. (II) are useful for modulating anginicantly delay the clotting time of normal human coagulants and significantly delay the clotting time of normal human coagulants and significantly delay the clotting time of normal human coagulating angiogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers for conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for modulating angiogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful for diagnostic reagents to detect the presence or absence of target substances to which they specifically bind, and for identifying substances to which they specifically bind, and for isolating and purifying substances to which they specifically bind. ABN88013 and ABBS121 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
factor activity, E2F activity and Angl or Ang2 activity in a mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Indels
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                                        Claim 13; Fig 1B; 216pp; English.
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l Similarity 77.1%;
74; Conservative (
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Best Local Similarity
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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoietin-I (Angi) or Angi, respectively, where (I), (II), (III) have a cardiant or angiopoietin-I (Angi) or Angi, respectively, where (I), (II) and (III) have a cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate is modulated. (I) are also useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting cell proliferation in a number of conditions e.g. intimal hyperplasia following bypass graft surgery. (III) are useful for inhibiting cell proliferation in a number of conditions e.g. intimal hyperplasia following bypass graft surgery. (III) are useful for research and therapeutic context. The aptamers are also useful for dagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic for research of they specifically bind, and for identifying substances to which they specifically bind. Abn8488 to Abs8713 and Abs88121 represent
                                                                                             Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 eggagagaagaagagauggececcaua-cecacuugcugcauceccuuccceuaaga 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA aptamer; identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis; bypass graft surgery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 95 BP; 25 A; 27 C; 28 G; 0 T; 15 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 6;
Pred. No. 4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                             Claim 13; Fig 1B; 216pp; English.
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Sullenger BA, Rusconi CP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 83.3
ses 80; Conservative
                                                  WPI; 2002-479560/51
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26-SEP-2001; 2001WO-US030004 26-SEP-2000; 2000US-0235654P

WO200226932-A2

Synthetic.

04-APR-2002

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The present invention describes RNA aptamers (I,IIII) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) andiopoietin-I (Angl) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family cardiant and cytostatic activities. (I) are useful for modulating the cardiant and cytostatic activities. (I) are useful for modulating the bloogical activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate is modulated. (I) are useful for modulating E2F cardiavascular diseases in the mammal. (II) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting cell proliferation in a number of conditions e.g., incimal hyperplasia following bypass graft surgery. (III) are useful for diagnostic consecul for inhibiting only propass graft surgery. (III) are useful for which they specifically bind, and for identifying substances to which they companies as esparation reagent for retrieving the targets to which they bind, and as a separation reagent for retrieving the targets to which they becifically bind. Angles to ABN88131 and ABBB3131 represent they sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                        Novel RNA aptamers that selectively bind coagulation pathway factors, Ez family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
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                                                                                                                                                                                                                                                                                                                                                                Claim 13; Fig 1A; 216pp; English.
26-SEP-2001; 2001WO-US030004
                                                 26-SEP-2000; 2000US-0235654P
                                                                                                                                                         CP;
                                                                                                                                                                                                          WPI; 2002-479560/51.
                                                                                                     (UYDU-) UNIV DUKE.
                                                                                                                                                      Sullenger BA,
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1 GGGAGAGGAAGAGGAUGGGCUAUAUACACGCUGGUGAUCCCAUCUCAAUUGAAACAA 60
                                                                                1 GGGAGAGAGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
                                            0; Gaps
61.7%; Score 59.2; DB 6; Length 96; 76.0%; Pred. No. 7.9e-12; ive 0; Mismatches 23; Indels
                                                                                                                                                                                     61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
                     Best_Local Similarity 76.0
Matches 73; Conservative
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RNA aptamer, identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis;
                                                                                              Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:12.
             ABN88499 standard; RNA; 95 BP
                                                                    (first entry)
                                                                                                                                                                       graft surgery; ss.
                                                                    19-AUG-2002
                                                                                                                                                                                                    sapiens
                                                                                                                                                                       bypass
                                                                                                                                                                                                  Homo
ABN88499
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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) a dissociation constant for the coagulation pathway factor, an E2F family cardiation constant for the coagulation pathway factor, an E2F family cardiating and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-coagular diseases in the mammal. (II) are useful for modulating E2F cardiovascular diseases in the mammal. (II) are useful for modulating anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting call profiferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for diagnostic. coseance and therapeutic context. The aptamers are useful for diagnostic, they specifically bind, and for identifying substances to which they copied, and as a separation reagent for retrieving the targets to which they bind, and as a separation reagent for shouls and Abundan Abunda and Abundan Abunda Abunda, and Abunda, 
                                                                                                                                                                                                                                                                                                                                                                                  Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGAGAGAGAGAGAGGGAUGGGGACUAUA-CGUGAACGACUGCAUCCACUUCCCCGCCAU 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95 BP; 25 A; 26 C; 29 G; 0 T; 15 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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0. Mismatches
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                                                                                                                                                                                                                                                                                            Rusconi CP;
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Best Local Similarity 82...
To 79; Conservative
                                                                                                                                                                                                                                                                                                                                            WPI; 2002-479560/51.
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aptamer; identification; coagulation factor; angiopoietin; thrombin; family; cardiant; cytostatic; cardiovascular disease; anticoagulant; proliferation; intimal hyperplasia; angiogenesis;

bypass graft surgery; ss.

Homo sapiens.

Synthetic.

RNA aptamer; E2F family; c

cell

26-SEP-2001; 2001WO-US030004 26-SEP-2000; 2000US-0235654P

WO200226932-A2

04-APR-2002

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Rusconi

Sullenger BA,

(UYDU-) UNIV DUKE.

WPI; 2002-479560/51.

Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:10.

(first entry)

19-AUG-2002

ABN88497;

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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoietin-1 (Angi) or Angi, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Angi or Angi of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate. (II) are useful for modulating cardiovascular diseases in the mammal. (II) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating cardiovasculants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for diagnostic research and therapeutic context. The aptamers are useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E2F
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RNA aptamer, identification, coagulation factor, angiopoietin, thrombin, E2F family, cardiant, cytostatic, cardiovascular disease, anticoagulant, cell proliferation, intimal hyperplasia, angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel RNA aptamers that selectively bind coagulation pathway factors, Ez family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 1A; 216pp; English.
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                                                                                bypass graft surgery; ss
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                                                                                                                                                     Synthetic.
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                                                                                        1 GGGAGAGGAAGAGGAAUGGGGACUAUACCGCGUAAAUGCUGCCUCCCCAUUCCGGAACG 60
                                                                                                                                    GGGAGAGAGGAAGAGGGAUGGGCACUAUA - CGCAUCTUGCUGCCUGCCCGCGAGUCAAU
                                                  1; Gaps
60.8%; Score 58.4; DB 6; Length 95; 82.3%; Pred. No. 1.6e-11; ive 0; Mismatches 16; Indels
                                                                                                                                                                               61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
                                                                                                                                                                                                                           95
                                                                                                                                                                                                        UGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC
                         Best Local Similarity 82.3
Matches 79; Conservative
    Query Match
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ABN88497 standard; RNA; 96 BP

ABN88497 ID ABN8 XX RESULT 8

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The present invention describes RNA aptamers (I,IIII) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) andiopoletin-I (Angl) or Angl, respectively, where (I), (II) have a candipoletin-I (Angl) or Angl, respectively, where (I), (II) have a dissociation constant for the coagulation pathway factor, an E2F family cardiant and cytostatic activities. (I) are useful for modulating the biological activity of the coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the blooded vertebrate is modulated. (I) are useful for treating cardiovascular diseases in the mammal. (II) are useful for modulating E2F cardiovascular diseases in the mammal. (II) are useful for modulating cardiovascular diseases in the mammal. (II) are useful for modulating and significantly delay the clotting time of normal human coagulation of platelets in response to thrombin. (II) are useful for intibiting cell proliferation in a number of conditions e g., intimal hyperplasia following bypass graft surgery. (III) are useful for intibiting angiogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful for diagnostic research and therapeutic context. The aptamers are useful for diagnostic reagents to detect the presence or absence of target substances to which they specifically bind, and for identifying substances to which they specifically bind. Abnaged to Abnagell substances to which they specifically bind. Abnaged to Abnagell substances to which they context of they specifically bind. Abnaged to Abnage and Abnagell substances to which they caparation reagent for retrieving the targets to which they caparation reagent for retrieving the targets to which they appeared to the present context. The aptencent intervent they appeared to the present context. The aptencent and therapeutic context. The aptencent and therapeutic context. The aptence to which they specifically bind. Abnaged to Abnage and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel RNA aptamers that selectively bind coagulation pathway factors, E2 family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 96 BP; 30 A; 25 C; 27 G; 0 T; 14 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 1A; 216pp; English.
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Best Local Similarity 74.0%;
Matches 71; Conservative
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Claim 13; Fig 1B; 216pp; English.
   BP.
                                                                                                                                                                                                                                                           58.3%;
                                                                                26-SEP-2001; 2001WO-US030004.
                                                                                        26-SEP-2000; 2000US-0235654P.
   ABN88500 standard; RNA; 96
                                                                                                        Sullenger BA, Rusconi CP;
                  (first entry)
                                              bypass graft surgery; ss.
                                                                                                                WPI; 2002-479560/51.
                                                                                                (UYDU-) UNIV DUKE
                                                                 WO200226932-A2
                                                      sapiens.
                  19-AUG-2002
                                                                         04-APR-2002
                                                         Synthetic.
          ABN88500;
                                                                                                                                                                                                                                                           Query Match
                                                      Homo
ABN88500
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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoletin-1 (Angl.) or Angl. respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Angl or Angl of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate. (II) are useful for modulating E2F activity in a warm-blooded vertebrate. (II) are useful for modulating cardiovascular diseases in the mammal. (III) are useful for modulating activity in a warm-blooded vertebrate. (II) are useful for modulating cardiovasculants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (III) are useful for inhibiting cell proliferation in a number of conditions of conting time of normal fundant warm-leads of conditions and an under of conditions of conting time of normal fundant warm the activation of platelets in response to thrombin. (III) are useful for inhibiting cell proliferation in a number of conditions of c
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                                                                                                                                                       RNA aptamer; identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis;
Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:13.
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Pred. No. 1.2e-10;
0; Mismatches 25; Indels
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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopotetin-I (Angi) or Angi, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family community of a coagulation pathway factor, an E2F family cardinistering of tytostatics. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate is modulating pathway factor in the warm-blooded vertebrate. (II) are useful for modulating E2F activity in a warm-blooded vertebrate. (III) are useful for modulating Cardiovascular diseases in the mammal. (II) are useful for modulating anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting call profiferation in a number of confictions of intimal hyperplasia following bypass graft surgery. (III) are useful for diagnostic research and therapeutic context. The aptamers are useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful so which they specifically bind, and for isolating aubstances to which they bind, and as a separation reagent for retrieving the targets to which they bind, and as a separation reagent for retrieving the targets to which they bind, and as a separation of the present invention
                                                                                                                                                                                                                                                                                                                                                                                              aptamer; identification; coagulation factor; angiopoietin; thrombin; family; cardiant; cytostatic; cardiovascular disease; anticoagulant; proliferation; intimal hyperplasia; angiogenesis;
Novel RNA aptamers that selectively bind coagulation pathway factors, E2 family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
                                                                                                                                                                                                                                                                                                                                                     Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:15.
                                                               61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC
                                                                                               61 UCCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Fig 1B; 216pp; English
                                                                                                                                                                                                                       ABN88502 standard; RNA; 96 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2001; 2001WO-US030004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2000; 2000US-0235654P
                                                                                                                                                                                                                                                                                                             19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sullenger BA, Rusconi CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bypass graft surgery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-479560/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                  ABN88502;
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0; Mismatches

Local Similarity 74.0

Matches

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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoletin; (Angi) or Angi, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Angi or Angi of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the obiological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that biological activity of the coagulation pathway factor in the warm-blooded vertebrate. (II) are useful for modulating cardiovascular diseases in the mammal. (II) are useful for modulating cardiovascular diseases in the mammal. (II) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating cardiovasculants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplasia following bypass graff surgery. (III) are useful for diagnostic research and therapeutic context. The aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
                                                                                 9
                                                                                                                    aptamer, identification; coagulation factor; angiopoietin; thrombin; family; cardiant; cytostatic; cardiovascular disease; anticoagulant; proliferation; intimal hyperplasia; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reagents to detect the presence or absence of target substances to which they specifically bind, and for identifying substances to which they
                                                                             GGGAGAGAGAAGAGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                        Coagulation factor VIIa binding/inhibiting RNA aptamer SEQ ID NO:40.
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    Length 96;
                                       26; Indels
                                                                                                                                                                                 61 UGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
    DB 6; L
2.8e-10;
                                                                                                                                                          61 CUCADAACCCAGAGGUCGADAGDACUGGAUCCCCCC
                                       0; Mismatches
    Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Fig 10; 216pp; English.
                                                                                                                                                                                                                                                                                                 ABN88527 standard; RNA; 96 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2001; 2001WO-US030004.
  57.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sullenger BA, Rusconi CP;
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bypass graft surgery; ss.
                                       Conservative
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                  Similarity
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Query Match
Best Local Simi
Matches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                           ABN88527;
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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (C) angiopoietin-I (Angi) or Ang2, respectively, where (I), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 nM or less (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that biological activity of the coagulation pathway factor in the warm-blooded vertebrate is modulated. (I) are also useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating and so activity in a warm-blooded vertebrate. (III) are useful for modulating anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aptamer; identification; coagulation factor; angiopoietin; thrombin; family; cardiant; cytostatic; cardiovascular disease; anticoagulant; l proliferation; intimal hyperplasia; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel RNA aptamers that selectively bind coagulation pathway factors, E2 family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
specifically bind, for isolating and purifying substances to which they bind, and as a separation reagent for retrieving the targets to which they specifically bind. ABM8448 to ABM89713 and ABB8121 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                 1 GGGAGAGAGAGGAGGAGGGGGCCAAAAGAGCUUCUUGUAGUAGAUCCCUCAACCGCA
                                                                                                                                                                                                                            1 GGGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coagulation factor X binding/inhibiting RNA aptamer SEQ ID NO:34.
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                                                                                                                                       Score 54.4; DB 6; Length 96;
Pred. No. 4.6e-10;
                                                                                                                                                                                    Indels
                                                                                                   Sequence 96 BP; 28 A; 22 C; 29 G; 0 T; 17 U; 0 Other;
                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                  61 AGCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
                                                                                                                                                                                                                                                                                                         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
                                                                                                                                                                                    0; Mismatches
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                                                                                                                                     56.7%;
72.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                          Local Similaricy
hes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bypass graft surgery; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN88521;
                                                                                                                                            Query Match
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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useful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for modulating angiogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic reagents to detect the presence or absence of target substances to which they specifically bind, and for identifying substances to which they becifically bind, for isolating and purifying substances to which they bind, and as a separation reagent for retrieving the targets to which they specifically bind. ABN88488 to ABN88713 and ABB81231 represent sequences used in the exemplification of the present invention
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Sequence 96 BP; 27 A; 29 C; 29 G; 0 T; 11 U; 0 Other;

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                                                                   1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
                                                                                                      1 GGGAGAGAGGAAGGGGAUGGGCCAGCAACCGAAGGGCGGAAUACCCCCGUCUCCACAUA 60
                                    Gaps
                                    ö
55.0%; Score 52.8; DB 6; Length 96; 71.9%; Pred. No. 1.8e-09;
                                  27; Indels
                                                                                                                                       96
                                                                                                                                                                       ccauaacccagaggucgauaguacuggauccccc 96
                                                                                                                                         61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC
                                  0; Mismatches
                Local Similarity 71.9
nes 69; Conservative
 Query Match
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Coagulation factor X binding/inhibiting RNA aptamer SEQ ID NO:23. ABN88510 standard; RNA; 96 (first entry) 19-AUG-2002 ABN88510;

RNA aptamer; identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis; bypass graft surgery; ss.

Homo sapiens. Synthetic.

WO200226932-A2

26-SEP-2001; 2001WO-US030004

04-APR-2002

26-SEP-2000; 2000US-0235654P

(UYDU-) UNIV DUKE,

Rusconi CP;

Sullenger BA,

WPI; 2002-479560/51.

Novel RNA aptamers that selectively bind coagulation pathway factors, E2 family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.

Claim 13; Fig 6A; 216pp; English.

The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoletin-1 (Angi) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-looded avertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-

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cardiovascular diseases in the mammal. [II] are useful for modulating E2F activity in a warm-blooded vertebrate. [III] are useful for modulating E2F activity in a warm-blooded vertebrate. [III] are useful for modulating D2F and or Angl activity in a warm-blooded vertebrate. [III] are useful for modulating control day the clotting time of normal human plasma or the activation of platelets in response to thrombin. [II] are useful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. [III] are useful for modulating angiogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic for farget specifically bind, and for identifying substances to which they specifically bind. Abs08448 to Abs08413 and Abs084231 represent context invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA aptamer; identification; coagulation factor; angiopoletin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes RNA aptamers (1,11,111) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoietin-1 (Angl) or Ang2, respectively, where (1), (11), (111) have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel RNA aptamers that selectively bind coagulation pathway factors, E2 family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:11.
for treating
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                                                                                                                                                                                                                                                                                                                                                                              Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                   28; Indels
                                                                                                                                                                                                                                                                                                                                       Sequence 96 BP; 29 A; 26 C; 28 G; 0 T; 13 U; 0 Other;
    blooded vertebrate is modulated. (I) are also useful
                                                                                                                                                                                                                                                                                                                                                                            Score 51.2; DB 6;
Pred. No. 6.9e-09;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Fig 1A; 216pp; English.
                                                                                                                                                                                                                                                                                                                                                                              53.3%;
70.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-2000; 2000US-0235654P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN88498 standard; RNA; 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E2F family; cardiant; cytucell proliferation; intimbypass graft surgery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rusconi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-479560/51.
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYDU-) UNIV DUKE
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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member, or Angl or Angl of about 20 mM or less. (1), (II) and (III) have cardiant and cytostatic activities. (1) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (1) to a warm-blooded vertebrate (e.g., a mammal) such that bloodical activity of the coagulation pathway factor in the warm-blooded vertebrate is modulated. (I) are also useful for modulating EZF activity in a warm-blooded vertebrate. (III) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating activity in a warm-blooded vertebrate. (III) are useful for modulating anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for intimal hyperplasia following bypass graft surgery. (III) are useful for modulating and herapetuic context. The aptamers are useful as diagnostic research and therapetuic context. The aptamers are useful as diagnostic reagents to detect the presence or absence of target substances to which they specifically bind, for isolating and purifying substances to which they specifically bind. AbbN88488 to AbbN88113 and AbbN881231 represent they specifically bind. AbbN88488 to AbbN88113 and present invention
  coagulation pathway factor, an E2F family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGAGAGAGGAAGGGGGAUGGGGAACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAGAGAGAGAGAGGGGAUGGGCUCAUCACAGGCGAAGUGAACAACACUACCGNCNAGUU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA aptamer; identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis; bypass graft surgery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel RNA aptamers that selectively bind coagulation pathway factors, E? family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:14.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.9%; Score 50.8; DB 6; Length 96; 69.8%; Pred. No. 9.6e-09; ive 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 96 BP; 29 A; 24 C; 28 G; 0 T; 13 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ACCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN88501 standard; RNA; 96 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001; 2001WO-US030004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rusconi CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 69.8
les 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sullenger BA,
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9, 2004, 03:17:44

Search completed: April Job time: 342.082 secs

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Claim 13; Fig 1B; 216pp; English.

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Chain 13; Fig 1B; 216pp; English.

XX

The present invention describes RNA aptamers (I,III) that selectively compliance of the coagulation pathway factor, an E2F family member; or (G) angiopoletin-1 (Angi) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family compliant and cytostatic activities. (I) are useful for modulating the cardinate and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves a marm-blooded vertebrate (e.g., a mammal) such that compliants error and second vertebrate is modulated. (I) are useful for modulating E2F cardivity in a warm-blooded vertebrate (e.g., a mammal) such that compliants and significantly delay the clotting time of normal human cardivity in a warm-blooded vertebrate. (I) are useful for modulating E2F cardivity in a warm-blooded vertebrate (III) are useful for modulating and or Ang2 activity in a warm-blooded vertebrate. (III) are useful for modulating and cardivity in a warm-blooded vertebrate (III) are useful for modulating angiogenesis following bypass graft surgery. (III) are useful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplass following bypass graft surgery. (III) are useful for diagnostic.

C anticoagulating angiogenesis. The RNA aptamers are useful as diagnostic.

C indulating angiogenesis. The RNA aptamers are useful as diagnostic.

C research and therapeutic context. The aptamers are useful as diagnostic.

C reagents to detect the presence or absence of target substances to which they bind, and as separation reagent for retrieving the targets to which they bind, and as a separation and puritying substances to which they be specifically bind, and as a separation and purity and the present invention

C sequences used in the exemplification of the present invention

AX

C sequences used in the exemplification of the present invention and
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us-09-963-827b-3. 200.rni

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 09-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994
PRIOR APPLICATION NUMBER: 08/117,991
FILING DATE: 08-SEPTEMBER-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
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                                                                                                                                          April 9, 2004, 02:54:20 ; Search time 78.6824 Seconds (without alignments) 677.093 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12,
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Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-512-861A-3
US-08-512-861A-5
US-08-512-861A-9
US-08-512-861A-4
US-08-512-861A-4
US-08-512-861A-10
US-08-512-861A-10
US-08-512-861A-11
US-08-512-861A-11
US-08-512-861A-13
US-08-512-861A-14
US-08-512-861A-15
US-08-512-861A-15
US-08-512-861A-15
US-08-512-861A-15
US-08-512-861A-15
US-08-512-861A-15
US-08-512-861A-16
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US-08-487-077A-40
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-08-485-862B-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                           682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*
                                                                                                                                                                                                                                                       US-09-963-827B-3
96
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Match Length
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Maximum DB seq length: 200
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                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                 OM nucleic
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                                                                                                                                                     Run on:
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No.
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APPLICANT: GOLD, LARRY
APPLICANT: NIEUANDT, DAN
APPLICANT: NIEUANDT, DAN
APPLICANT: WECKER, MATTHEW
APPLICANT: SCHNEIDER, DANIEL J.
APPLICANT: FEIGON, JULI
APPLICANT: ALLEN, PARTECK
APPLICANT: ALLENGER, BRUCE A.
APPLICANT: DOUDNA, JENNIFER, A.
APPLICANT: DOUDNA, JENNIFER, A.
TITLE OF INVENTION: HIGH-APFINITY LIGANDS OF
TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 239
                                                                                                                                                                                                                  Sequence
Seq
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                      Sequence
Sequence
Sequence
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Sequence
Sequence
US-08-485-863A-40
US-08-485-049D-40
US-09-178-115-40
US-09-177-776-40
PCT-US95-05600-114
PCT-US95-05600-113
US-08-488-402A-97
US-08-488-52A-97
US-08-448-52A-97
US-08-443-52A-97
US-08-443-52A-97
US-08-443-762A-94
PCT-US95-05600-15
PCT-US95-05600-15
PCT-US95-05600-17
PCT-US95-05600-17
PCT-US95-05600-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Swanson & Bratschun, L.L.C. 8400 E. Prentice Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application PC/TUS9505600 GENERAL INFORMATION: APPLICANT: GOLD, LARRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,863
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,632
FILING DATE: 24-MAY-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
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    ADDRESSEE:
STREET: 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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PCT-US95-05600-12
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Gaps

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29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCCAGAGGUCGAUAGUACUGG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ACAGCAGAGUGGCGCAGCGAAGCGUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.7%; Score 21.8; DB 3; Length 108; Best Local Similarity 58.5%; Pred. No. 40; Matches 38; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: James D. THOMPSON
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FeatSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146866ember 10, 1994
ATTORNEY AGENT INFORMATION:
NAME: WATORUS, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 215/154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                               NAME: Warburg, Richard
REGIGTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 215/154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELERAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-512-861A-7; Sequence 7, Application US/08512861A; Patent No. 6146886
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TELEPHONE: (213) 969-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 AUCCC 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.6%; Score 23.6; DB 5; Length 87; Best Local Similarity 63.1%; Pred. No. 7.8; Matches 53; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08512861A
Sequence 1, Application US/08512861A
Sequence 1, Application US/08512861A
Sequence 2, Application US/08512861A
GENERAL INFORMATION:
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
CORRESPONDENCES. 25
CORRESPONDENCES. 25
STREET: 630 West Fifth Street
STREET: 631 West Fifth Street
STREET: California
STREET: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.0 Diskette, 1.44 Mb
SOFTWARE: 18M Compatible
COMPUTER: 18M Compatible
COMPUTER: 18M COMPUTER: 18M
                   PRIOR APPLICATION DATA:
PRING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
PRING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
PRING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: BATTY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX17/PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (303) 793-333
TELEFAX: (303) 793-333
TELEFAX: (303) 793-333
TELEFAX: BASE DATE: 12:
ENGTHEN 87 BASE DATE
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 CGCUCAUAACCCAGAGGUCGAUAG 82
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   APPLICATION NUMBER: 07/931,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear PCT-US95-05600-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-512-861A-3
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TOPOLOGY: linear

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29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
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Patent No. 6146886
GENERAL James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: IMPROVED RNA FOLKESTORE STANDARES: 25
ADDRESSE: Lyon & Lyon & Lyon & Lyon & Lyon & Lyon & THERT: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.0M
SOFTWARE: 10M PATE: 10M P.C. DOS 5.0
SOFTWARE: ApplICATION DATA: 4.1995
FILING DATE: August 8, 1995
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: NO. 6146866mber 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WALCHAUF, RICHARD
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 215/154
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21.8; Di
Pred. No. 43;
0; Mismatches
                                                                                                   Sequence 9, Application US/08512861A
Patent No. 6146886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67.3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.5
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-512-861A-9
                                                                                                                                                    GENERAL INFORMATION:
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                                                          RESULT 5
US-08-512-861A-9
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US-08-512-861A-4
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                                                                                                                                                      29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
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                                                                                                             Gaps
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                                                          Score 21.8; DB 3; Length 109;
Pred. No. 41;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.7%; Score 21.8; DB 3; Length 133; 58.5%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 614686
GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: CALLILLIAND
ZIP: 90071
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 815" Diskette, 1.44 Mb
SOFTWARE: IBM Compartible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/093,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/293,520
FILING DATE: No. 6146886ember 10, 1994
ATOMNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REBERENCE/DOCKET NUMBER: 215/154
TELECOMOUNICATION INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: 67-3310
TELEFAX: 67-3310
STENDENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08512861A
                                                       Query Match 22.7%;
Best Local Similarity 58.5%;
Matches 38; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.5'
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                89 AUCCC 93
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US-08-512-861A-7
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29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCCAGAGGUCGAUAGUACUGG 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08512861A

Patent No. 6146886
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALF 900'D.

CALF 900'D.

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CALF 900'D.

MEDIUM TYPE: S.S. Diskette, 1.44 Mb MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASISCO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NATA: 1995
PRIOR APPLICATION DATA: Two
APPLICATION NAMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/293,520
FILING DATE: No. 6146886mber 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION INFORMATION:
REGISTRATION NUMBER: 32,327
                                                           PELECTION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIOR APPLICATION DATA: Two
PRIOR APPLICATION DATA: Two
PRIOR APPLICATION DATA: Two
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886ember 10, 1994
ATTONNEY AGENT INFORMATION:
NAME: Warburg, Richard
ATTONNEY AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90071
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US-08-512-861A-8
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US-08-512-861A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ACAGCAGAGUGGCGCAGCGGAAGCGUGCGGCCCAUAAACCCCAGAGGGUCGAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.7%; Score 21.8; DB 3; Length 146; Best Local Similarity 58.5%; Pred. No. 45; Matches 38; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: INFROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                 MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PILING DATE: August 19, 1994
APPLICATION NUMBER: 08/293,520
FILING DATE: No. 6416886mber 10, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6416886mber 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 215/154
TELECOMMUNICATION INFORMATION:
TELEPRONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146
THENDER: A16
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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SYSTEM: IBM P.C. DOS 5.0
FastSEQ Version 1.5
STREET: Lyon & Lyon STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08512861A
Patent No. 6146886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FASTSEQ
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us-09-963-827b-3._200.rni

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NAME/KEY: uneure

| LOCATION: 18, 30, 35, 39, 44, 52, 87, 93, 108, 112, 114, 151, 166, 168, 170

| OTHER INFORMATION: a, t, c, g, or other

US-03-919-172-11
                                                                                    29 ACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUGG 88
                                                                                                                                                       7 ACAGCAGAGUGGCGCGGAAGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAA 66
              Gaps
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Patent No. 6346385

GENERAL INFORMATION:

ADPLICANT:

TITLE OF INVENTION:

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Pred. No. 80;
6; Mismatches 27; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 107;
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Best Local Similarity 50.9%; Pred. No. 57;
Matches 28; Conservative 6; Mismatches 21; Indels
              Mismatches 27; Indels
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OTHER INFORMATION: Incyte ID No. 6673545 378497.1
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Fatent No. 6673545
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
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              38; Conservative
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Best Local Similarity 46.8
Matches 29; Conservative
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LENGTH: 176
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-581-617-1
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SOFTWARE: Patentin Ve.
SEQ ID NO 1
LENGTH: 107
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US-09-919-172-11
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              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 171;
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Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION:
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BAA
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
RIOR APPLICATION NUMBER: 08/293,520
FILING DATE: Nugust 19, 1994
APPLICATION NUMBER: 08/293,520
FILING DATE: No. 6146886ember 10, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: Number: 08/4337,608
FILING DATE: 08/4337,608
                                                                                                                                                                                                                                                                                                                                                                                               Query Match · 22.7%; Score 21.8; DB
Best Local Similarity 58.5%; Pred. No. 47;
Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
       (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.7%;
58.5%;
TELEPHONE: (213) 489-160
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (213) 955-0440
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 171
                                                                                                                                                                                                                  TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-512-861A-6
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STATE: California
COUNTRY: U.S.A.
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Best Local Similarity
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                                                                                                                                                                             LENGTH:
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Patent No.
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                                          19 UGGGGACUAUACCGCGUAAUGCUGCCCCCCAUUCCGGAACGCUCAUAACCCAGAGGUCG 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Shite 4700
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ZIP: 90071

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: LIBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FESTENGO VERSION 1.5
CURRENT APPLICATION DATA: TWO
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
RIOR APPLICATION NUMBER: 08/293,520
FILING DATE: NAUGHT 19, 1994
APPLICATION NUMBER: 08/293,520
FILING DATE: NO. 6146886ember 10, 1994
APPLICATION NUMBER: 22,327
REFERENCE/DOCKET NUMBER: 215/154
TELECOMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 215/154
TELECOMUNICATION INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-512-861A-13
; Sequence 13, Application US/08512861A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08512861A Patent No. 6146886
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Best Local Similarity 56.73
Matches 38, Conservative
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STATE: California
COUNTRY: U.S.A.
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                              LS4 GT 155
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US-08-512-861A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                           IMPRÔVED RNA POLYMERASE III-BASED EXPRESSION OF THERAPEUTIC RNAS
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5 EACTAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRANCE OF STORM 1.5
CURRENT APPLICATION INDATA: Two
APPLICATION NUMBER: 08/08/51,861A
FILING DATE: NO. 614686 ember 10, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: NO. 6146886 ember 10, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: NO. 6146886 ember 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
RESERENCE/DOCKET NUMBER: 215/154
TELECOMMUNICATION INFORMATION:
               APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA FITLE OF INVENTION: EXPRESSION OF NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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STREET: 633 West Fifth Street
STREET: Suite 4700
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213)
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Best Local Similarity 56.73
Matches 38; Conservative
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STRANDEDNESS: sing
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
GENERAL INFORMATION:
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Search completed: April 9, 2004, 06:07:31 Job time : 81.6824 secs
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 46.3
Matches 25; Conservative
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VECTORS UTILIZING A SINGLE RNA POLYMERASE FOR BOTH
DIRECTIONS
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ZUP: 01915

COMPTON TO THE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ParentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,640

***TING DATE: 18-MAY-1995
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21.5%; Score 20.6; DB 3;
Best Local Similarity 56.7%; Pred. No. 1.3e+02;
Matches 38; Conservative 0; Mismatches 29;
COMPUTER READBABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: FASTEN: IBM P.C. DOS 5.0
SOFTWARE: FASTEN: IBM P.C. DOS 5.0
SOFTWARE: FASTEN: IBM P.C. DOS 5.0
SOFTWARE: FASTENIN DATA:
APPLICATION NUMBER: US/08/512,861A
APPLICATION NUMBER: 08/293,520
FILING DATE: AUGUST 19, 1994
APPLICATION NUMBER: 08/293,500
FILING DATE: No. 6146866mber 10, 1994
APPLICATION NUMBER: 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WAZDUTTON INFORMATION:
TELEPHONE; (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08443640
| Patent No. 5691140
| GENERAL INFORMATION:
| APPLICANT: NOREN, CHRISTOPHER J.
| TITLE OF INVENTION: BIDIRECTIONAL IN VIT.
| TITLE OF INVENTION: DIRECTIONS |
| TITLE OF INVENTIONS |
| TI
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 167
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Gaps
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                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                                      8; Mismatches
             REFERENCE/DOCKET NUMBER: NEB-
TELECOMMUNICATION INFORMATION:
TELEPAX: (508) 927-5054
TELEPAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 base pairs
TYPE: nucleic acid
30901
REGISTRATION NUMBER:
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Appl Appl Appl Appl Appl Appl Appl

Sequence Sequence Sequence Sequence Sequence Sequence

Scoring table:

Total number

Database

Searched:

Perfect score:

Sequence:

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Run on:

Sequence Sequence Sequence Sequence

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Sequence Sequence

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Sequence 3, Application US/09963827B
; Sequence 3, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Duke University
; APPLICANT: Sullenger, Bursconi, Christopher
; TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
; FILE REPRENCE: 180/124/2
; CURRENT APPLICATION NUMBER: US/09/963,827B
; CURRENT FILING DATE: 2000-09-26
; PRIOR FILING DATE: 2000-09-26
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ IN NOS: 227
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGAGAGAGAGAGAGAGGGAUGGGGAUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG
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US-09-963-827B-14

US-09-963-827B-16

US-09-963-827B-31

US-09-963-827B-41

US-09-963-827B-41

US-09-963-827B-42

US-09-963-827B-43

US-09-963-827B-23

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US-09-963-827B-45

US-09-963-827B-47

US-09-963-827B-31

US-09-963-827B-34

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US-09-963-827B-33
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NAME/KEXY: RNA aptamer
LOCATION: (1)..(96)
OTHER INFORMATION: RNA aptamer
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OTHER INFORMATION: RNA aptamer
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ORGANISM: Artificial Sequence
    Query Match
Best Local Similarity
Matches 96; Conserv
                           US-09-963-827B-3
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49.6
49.6
69.6
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Appli
                                                                                                       (without alignments)
303.112 Million cell updates/sec
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Sequence
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Sequence 6
Sequence 9
                                                                                         April 9, 2004, 03:53:35 ; Search time 1188.14 Seconds
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| Cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_PUBF_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_PUBF_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO08_PUBCOMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-963-827B-19
US-09-963-827B-17
US-09-963-827B-2
US-09-963-827B-4
US-09-963-827B-12
US-09-963-827B-12
US-09-963-827B-13
US-09-963-827B-15
US-09-963-827B-15
US-09-963-827B-15
US-09-963-827B-15
US-09-963-827B-16
US-09-963-827B-11
US-09-963-827B-11
US-09-963-827B-11
US-09-963-827B-11
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Maximum Match 100%
Listing first 45 summaries
                                                                  - nucleic search, using sw model
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Match Length
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Maximum DB seq length: 200
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60.8 59.2 58.4 58.4 56.5 56.8 56.8

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1 GGGAGAGAGAGGAGGAGGAGGAGAGAGAGAACCGGCAAUCGUGCAUCCCCUGGACCUAACAA 60
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                                                                      1 GGGAGAGAGGAAGGAGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
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Fublication No. US20030175703A1

GENERAL INFORMATION:

APPLICANT: Duke University

APPLICANT: Sullenger, Bruce

APPLICANT: Rusconi, Christopher

TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME

FILE REFERENCE: 180/124/2

CURRENT APPLICATION NUMBER: US/09/963,827B

CURRENT FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 227

SOFTWARE: PALENTIN OOS: 227

SOFTWARE: PALENTIN OF SEQ ID NOS: 227

SEQ ID NO 2

LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Duke University
APPLICANT: Duke University
APPLICANT: Bulenger, Bruce
APPLICANT: Rusconi, Christopher
ITILE OF INVENTION: RNA APTARES AND METHODS FOR IDENTIFYING THE SAME
FILE REFERENCE: 180/124/2
CURRENT APPLICATION UNMBER: US/09/963,827B
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,654
PRIOR APPLICATION NUMBER: 60/235,654
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
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                         Indels
Best Local Similarity 77.1%; Pred. No. 3.4e-13; Matches 74; Conservative 0; Mismatches 22;
                                                                                                                                                                        61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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Pred. No. 6.8e-13;
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                                                                                                                                                                                                                                                                                                                                        ; Sequence 22, Application US/09963827B; Publication No. US20030175703A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)..(55)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-22
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.39
Warrhes 80; Conservative
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US-09-963-827B-22
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LENGTH: 95
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APPLICANT: DUACE University
APPLICANT: Sullenger, Bruce
APPLICANT: Rusconi, Christopher
TITLE OF INVENTION: RAPTAMERS AND METHODS FOR IDENTIFYING THE SAME
TITLE OF INVENTION: RAPTAMERS AND METHODS FOR IDENTIFYING THE SAME
TILE REFERENCE: 180/124/2
CURRENT APPLICATION NUMBER: US/09/963,827B
CURRENT FILING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 94
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Publication No. US20030175703A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Duke University
APPLICANT: Sullenger, Bruce
APPLICANT: Rusconi, Christopher
ITILE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
FILE REFERENCE: 1801/22/2
CURRENT FILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
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     61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCCC 96
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                                                                                                                        Sequence 19, Application US/09963827B Publication No. US20030175703A1
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LOCATION: (1)..(194)
... OTHER INFORMATION: RNA aptamer
US-09-963-8278-19
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OTHER INFORMATION: RNA aptamer
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LOCATION: (1)..(96)
OTHER INFORMATION: RNA aptamer
US-09-963-8278-17
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SOFTWARE: Patentin version 3.0
SEQ ID NO 196
LENGTH: 96
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 78.74
Matches 74; Conservative
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US-09-963-827B-17
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Query Match

TYPE: RNA

FEATURE:

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RESULT 9
US-09-963-827B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence 4, Application US/09963827B | Sequence 4, Application No. US20030175703A1 | Septence 4, Application No. US20030175703A1 | GENERAL INFORMATION: APPLICANT: Duke University | APPLICANT: Bulenger, Bruce | APPLICANT: Rusconi, Christopher | TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME | FILE REFERENCE: 180/124/2 | CURRENT APPLICATION NUMBER: US/09/963,827B | CURRENT PILING DATE: 2001-09-26 | PRIOR APPLICATION NUMBER: 60/235,654 | PRIOR FILING DATE: 2000-09-26 | NUMBER OF SEQ ID NOS: 227 | SOFTWARE: Patentin version 3.0 | SEQ ID NO 4 | LENGTH: 95
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Publication No. US20030175703A1
GENERAL INFORMATION:
APPLICANT: Duke University
APPLICANT: Sullenger, Bruce
APPLICANT: Rusconi, Christopher
ITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
FILE REFERENCE: 180/124/2
CURRENT APPLICATION NUMBER: US/09/963,827B
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                                                                                                                                                             Length 96;
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                                                                                                                                                           ; DB 10;
1.4e-12;
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                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                         Score 59.2;
Pred. No. 1.
                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(96)
CTHER INFORMATION: RNA aptamer
US-09-963-827B-2
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LOCATION: (1)...(95)
OTHER INFORMATION: RNA aptamer
US-09-963-827B-4
INFORMATION: RNA aptamer
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                                                                                                                                                         Query Match 61.7%;
Best Local Similarity 76.0%;
Matches 73; Conservative
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Sequence 10, Application US/09963827B
Sequence 10, Application No. US20030175703A1
GENERAL INFORMATION
APPLICANT: Duke University
APPLICANT: Rusconi, Christopher
APPLICANT: Rusconi, Christopher
TITLE OF INVENTION: RA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
FILE REFERENCE: 180/124/2
CURRENT APPLICATION NUMBER: 60/235,654
PRIOR PLILING DATE: 2001-09-26
PRIOR PLILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
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Pred. No. 2.2e-11;
0; Mismatches 25; Indels
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION UNMBER: 60/235,654
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 95
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LOCATION: (1)..(95)
OTHER INFORMATION: RNA aptamer
US-09-963-827B-12
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LOCATION: (1)...(96)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-10
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                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
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illarity 74.0%;
Conservative (
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-963-827B-10
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LENGTH: 96
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Matches
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Publication No. US20030175703A1

GENERAL INFORMATION:

APPLICANT: Duke University

APPLICANT: Sullenger, Bruce

APPLICANT: Sullenger, Bruce

APPLICANT: Rusconi, Christopher

TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME

FILE REFERENCE: 180/124/2

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/235,654

PRIOR PLING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 227

SOFTWARE: Patentin version 3.0
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                                                              APPLICANT: Duke University
APPLICANT: Duke University
APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Bruce
APPLICANT: Rusconi, Christopher
TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
FILE REFERENCE: 180/124/2
CURRENT APPLICATION NUMBER: 08/926
PRIOR APPLICATION NUMBER: 60/235,654
PRIOR PILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
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Pred. No. 2.2e-11;
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Sequence 13, Application US/09963827B Publication No. US20030175703A1 GENERAL INFORMATION:
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NAMEKEY: misc feature
LOCATION: (1)..(96)
COTHER INFORMATION: RNA aptamer
US-09-963-8278-13
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; OTHER INFORMATION: RNA aptamer
US-09-963-8278-15
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74.0%;
                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 74.0°
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LOCATION: (54)...(54)
OTHER INFORMATION: n=c or
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LENGTH: 96
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Length 96;

Score 55; DB 10; Pred. No. 5.3e-11;

57.3%; 72.9%;

Query Match Best Local Similarity

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US-09-963-827B-40

US-09-963-827B-40

Sequence 40, Application US/09963827B

Publication No. US20030175703A1

SEQUENCE INFORMATION:

APPLICANT: Duke University

APPLICANT: Sullenger, Bruce

APPLICANT: Rusconi, Christopher

TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME

TITLE OF INVENTION: RNA APTAMERS: US/09/963,827B

CURRENT FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 227

SOFTWARE: Patentin version 3.0

SEQ ID NO 40

LUSTON APPLICATION OF 40
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      Gaps
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Publication No. US20030175703A1
GENERAL INFORMATION:
APPLICANT: Duke University
APPLICANT: Sullenger, Bruce
APPLICANT: Rusconi, Christopher
FILE REFERENCE: 180/1242
CURRENT APPLICATION NUMBER: US/09/963,827B
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      26; Indels
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llarity 72.9%; Pred. No. 9e-11;
Conservative 0; Mismatches 26;
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      0; Mismatches
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PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 96
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LOCATION: (1)..(96)
CHER INFORMATION: RNA aptamer
US-09-963-827B-40
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
      70; Conservative
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Best Local Similarity
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1 GGGAGAGAGAGGGGAUGGGCGAUAACCAACAUGGUGAUCCCAUUCAUCAUACCCUAC 60
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APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Bruce
APPLICANT: Nameoni, Christopher
TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
FILE REFERENCE: 180/124/2
CURRENT APPLICATION NUMBER: 05/09/963,8278
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,654
PRIOR APPLICATION NUMBER: 60/235,654
RUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
  TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
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Pred. No. 6e-09;
0; Mismatches 29; Indels
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Pred. No. 6e-09;
0; Mismatches 29;
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                        FILE REFERENCE: 180/124/2
CURRENT APPLICATION NUMBER: US/09/963,827B
CURRENT FILING DATE: 2001-09-26
                                                      PRIOR APPLICATION NUMBER: 60/235,654
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 96
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                                                                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(96)

CHER INFORMATION: RNA aptamer
US-09-963-827B-6
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OTHER INFORMATION: RNA aptamer
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; OTHER INFORMATION: RNA aptamer
US-09-963-827B-9
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69.8%;
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.8<sup>1</sup>
Matches 67; Conservative
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Publication No. US20030175703A1
GENERAL INFORMATION:
APPLICANT: Duke University
APPLICANT: Sullenger, Bruce
APPLICANT: Rusconi, Christopher
TITLE ROFINGATION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
CURRENT APPLICATION NUMBER: US/09/963,827B
CURRENT FILING DATE: 2001-09-26
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                                                                                                                                                           Query Match 53.3%; Score 51.2; DB 10; Best Local Similarity 70.8%; Pred. No. 1.5e-09; Matches 68; Conservative 0; Mismatches 28;
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Pred. No. 2.
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PRIOR FILING DATE: 2001-926
NUMBER OF SEQ ID NOS: 227
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                   FEATURE:

MAME/KEY: misc feature

LOCATION: (1)...(96)

OTHER INFORMATION: RNA aptamer
US-09-963-8278-23
OTHER INFORMATION: RNA aptamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(96)
OTHER INFORMATION: RNA aptamer
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OTHER INFORMATION: n=c, u or
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Best Local Similarity 69.8%;
Matches 67; Conservative
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Length 96;

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Indels

Search completed: April 9, 2004, 10:11:30 Job time: 1190.14 secs

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Sequence 28742, Application US/10793479 GENERAL INFORMATION:
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US-10-793-479-28742
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                                                                                                                                                                                                    April 9, 2004, 03:18:00 ; Search time 306.071 Seconds (without alignments) 200.961 Million cell updates/sec
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1. /cgn2 6/ptodata/2/pna/USO6_NEW_COMB.seq:*

1. /cgn2 6/ptodata/2/pna/USO6_NEW_COMB.seq:*

1. /cgn2 6/ptodata/2/pna/USO7 NEW COMB.seq:*

1. /cgn2 6/ptodata/2/pna/USO9_NEW_COMB.seq:*

2. /cgn2 6/ptodata/2/pna/USO9_NEW_COMB.seq:*

2. /cgn2 6/ptodata/2/pna/USO9_NEW_COMB.seq:*

3. /cgn2 6/ptodata/2/pna/USO9_NEW_COMB.seq:*

3. /cgn2 6/ptodata/2/pna/USO9_NEW_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-803-180-1491
US-10-803-180-1490
US-10-803-180-1496
US-10-803-180-1496
US-10-803-180-1496
US-10-793-479-10298
US-10-793-479-10298
US-10-793-479-10298
US-10-793-180-1494
US-10-803-180-1494
US-10-803-180-1495
US-10-767-791-19121
US-10-767-791-19121
US-10-767-701-19121
US-10-767-701-19121
US-10-767-701-19121
US-10-785-782-2966
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US-10-785-782-2966
US-10-785-782-2966
US-10-783-479-14465
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Maximum Match 100%
Listing first 45 summaries
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seg lèngth: 200
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Maximum DB
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Sequence 1281, Ap
Sequence 24133, A
Sequence 21521, A
Sequence 21521, A
Sequence 19905, A
Sequence 19305, A
Sequence 18305, A
Sequence 1610, Ap
Sequence 26801, A
Sequence 2108, A
Sequence 11813, A
Sequence 12941, A
Sequence 1705, Ap
Sequence 1705, Ap
Sequence 6705, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc_feature
; LOCATION: 12, 19, 35, 50, 51, 52, 67, 89, 90, 117, 118, 122, 129, 133,
; LOCATION: 144, 163
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Burges, Christopher C.
APPLICANT: Burges, Christopher C.
APPLICANT: Astle, Jon H.
APPLICANT: Carroll, Eddie III
APPLICANT: Carroll, Redie III
APPLICANT: Carroll, Redie III
APPLICANT: Dwivedi, Poornima
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Nucleic Acid Sequences Differentially
TITLE OF INVENTION: Sexpressed in Cancer Tissue
FILE REPERENCE: 1657/1032
CURRENT FILING DATE: 2001-10-02
FRIOR FILING DATE: 2000-02-10
FRIOR FILING DATE: 2000-02-10
FRIOR FILING DATE: 2000-02-10
SEQ ID NO S: 4494
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1175
US-10-785-782-1281

US-10-783-479-24133

US-10-793-479-21521

US-10-793-479-21521

US-10-793-479-22764

US-10-793-479-19905

US-10-793-479-19905

US-10-793-479-18124

US-10-785-782-1980

US-10-785-782-1980

US-10-785-782-12949

US-10-786-782-12949

US-10-786-782-12949

US-10-786-782-12949

US-10-786-782-12949

US-10-786-782-12949

US-10-786-782-12949

US-10-786-782-12949

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US-10-788-782-12949

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US-10-788-782-12949
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1158
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1100
1100
1130
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ORGANISM: Homo sapiens
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US-09-969-034-110/c
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TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REC
CURRENT APPLICATION NUMBER: US/09/513,999
PRIOR APPLICATION NUMBER: US/09/513,999
PRIOR APPLICATION NUMBER: US/09/513,999
PRIOR PLING DATE: 1099-02-24
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 13386
LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 VGGGGACUAVACCGCGUAAVGCUGCCUCCCCAVUCCGGAACGCUCAVAACCCAGAGGUCG 78
               APPLICANT: Duclert, A. A. APPLICANT: Duclert, A. APPLICANT: Duclert, A. TITLE ON THE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. TITLE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US/10/793,479
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US/09/513,999
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: PATENT. DM
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TAPLICANT: Glordano, J.Y.
TILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                20.6%; Score 19.8; DB 6; 38.1%; Pred. No. 2.9e+02; iive 12; Mismatches 27
Dumas Milne Edwards, J.B
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.1%
Matches 24; Conservative
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Best Local Similarity 49.1:
Matches 27; Conservative
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CRGANISM: Homo sapiens
US-10-793-479-13386
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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US-10-793-479-13386/c
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151 TTA 153
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US-10-793-479-8881/c
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Sequence 1481, Application US/10803180

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001511
CURRENT APPLICATION NUMBER: US/10/803,180
CURRENT FILING DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 6676
SOFTWARE: PastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001511
CURRENT APPLICATION NUMBER: US/10/803,180
CURRENT FILING DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 6676
SSOTWARE: FastSEQ for Windows Version 4.0
ENGTH: 155
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Pred. No. 3.4e+02;
4; Mismatches 14; Indels
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Pred. No. 3.9e+02;
4; Mismatches 16; Indels
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CURRENT APPLICATION NUMBER: US/10/793,479;
CURRENT FILING DATE: 2004-03-03;
PRIOR APPLICATION NUMBER: US/09/513,999;
PRIOR FILING DATE: 2000-02-24;
PRIOR APPLICATION NUMBER: US 60/122,487;
PRIOR FILING DATE: 1999-02-26;
NUMBER OF SEQ ID NOS: 36681;
SOFTWARE: Patent.pm;
SOFTWARE: Patent.pm;
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20.2%;
Best Local Similarity 55.6%;
Matches 25; Conservative 4
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Best Local Similarity 57.1%;
Matches 24; Conservative
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US-10-793-479-8881
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                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 12
OTHER INFORMATION: 8=9
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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US-10-803-180-1481
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LENGTH: 155
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Gaps

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APPLICANT: Leach, Martin
APPLICANT: Estach, Martin
APPLICANT: Estach, Martin
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Metirite OF INVENTION: Use Thereof
FILE REFERENCE: 15966-611
CURRENT APPLICATION NUMBER: US/10/785,782
CURRENT FILING DATE: 2004-02-23
PRIOR APPLICATION NUMBER: US/09/755,374
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 28742
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1479, Application US/10803180
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TUTLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NAMBER: US/10/803,180
CURRENT APPLICATION NAMBER: US/10/803,180
CURRENT PILING DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 6676
SOFTWARE: FREUSE OF OF WINDOWS Version 4.0
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OTHER INFORMATION: 1 of 2 allelic variants (6108 is other entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     95 raaaggritaaccccaarcccaagrgcrgaaaaccagaggcrga 51
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Pred. No. 4.1e+02;
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FILE REFERENCE: CL001511
CURRENT APPLICATION NUMBER: US/10/803,180
CURRENT FILING DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 6676
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1496
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Best Local Similarity 55.6%;
Matches 25, Conservative
                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1496
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CORGANISM: Homo sapiens
US-10-803-180-1479
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ORGANISM: Homo sapiens
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US-10-785-782-6107/c
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEDWATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001511
CURRENT APPLICATION NUMBER: US/10/803,180
CURRENT FILING DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 6676
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOUSII.
CURRENT APPLICATION NUMBER: US/10/803,180
CURRENT FILING DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 6676
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1488
LENGTH: 182
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
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                                                                               Score 19.4; DB 6; Length 155;
Pred. No. 3.9e+02;
4; Mismatches 16; Indels
                                                                                                                                                                                   35 UNAUGCUGCCUCCCAUUCCGGNACGCUCAUAACCCAGAGGUCGA 79
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Pred. No. 3.9e+02;
4; Mismatches 16;
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GENERAL INFORMATION:
                                                                            Query Match 20.2%;
Best Local Similarity 55.6%;
Matches 25; Conservative
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Best Local Similarity 55.6%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-10-803-180-1472
     ; ORGANISM: Homo sapiens
US-10-803-180-1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-803-180-1488
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LENGTH: 156
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Sequence 1484, Application US/10803180
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001511
CURRENT APPLICATION NUMBER: US/10/803,180
CURRENT APPLICATION NUMBER: US/10/803,180
CURRENT FILING DATE: 2004-03-18
NUMBER OF SEQ ID NOS: 6676
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/10/793,479
CURRENT PILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 33426
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                                                                                                                                   Query Match 19.8%; Score 19; DB 6; Best Local Similarity 60.0%; Pred. No. 3.9e+02; Matches 21; Conservative 4; Mismatches 10
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55.6%; Pred. No. 5.9e+02;
tive 4; Mismatches 16
                                                ; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43955877
US-10-785-782-8362
                                                                                                                                                                                                                                                      61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC
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Pred. No. 5.7e4
4; Mismatches
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52.9%;
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Best Local Similarity 55.6
Matches 25; Conservative
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                         NAME/KEY: misc_feature LOCATION: (0)...(0)
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CORGANISM: Homo sapiens
US-10-803-180-1484
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nes 27; Conserv
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APPLICANT: Leach, Martin
APPLICANT: Leach, Martin
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meth
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 15966-611
CURRENT PILLNG DATE: 2004-02-23
PRIOR APPLICATION NUMBER: US/09/755,374
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 28742
LENGTH: 51
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APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TILE GIORDANC, J.Y.
TILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/10/793,479
CURRENT FILING DATE: 2004-03-03
PRIOR PLICATION NUMBER: US/09/513,999
PRIOR PLICATION NUMBER: US 60/122,487
PRIOR PLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 10298
LENGTH: 160
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LOCATION: (26) ...(0)
OTHER INFORMATION: 2 of 2 allelic variants (8361 is other entry)
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                                                                                            Length 51;
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                                                                                                                                     6; Mismatches 13; Indels
                                                                                                                                                                                 54
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                                                                                                                                                                                 15 GGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCC
                                                                                       Score 19.2; DB 6;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19.2; DB 6;
Pred. No. 4.7e+02;

    LOCATION: (0) ...(0)
    OTHER INFORMATION: Accession number cg43986469
US-10-785-782-6107

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GENERAL INFORMATION:
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                                                                                       Query Match 20.0%;
Best Local Similarity 52.5%;
Matches 21; Conservative
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Best Local Similarity 53.6%;
Matches 30; Conservative
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US-10-793-479-10298
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-785-782-8362
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Run on:

Sequence:

Minimum DB Maximum DB

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Mus musculus (house mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Bun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weise,R.

Robilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weise,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weise

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Fax: 801 585 7177
                                                                                                                                            AQS45235 CITBI-EI-
BY317529 BY317529
CD150229 ML1-0019T
AQ537838 RPCI-11-3
BIO33417 QV3-ET017
CG559758 OST179226
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BF486945 ATZ135-5
AV173481 AV173481
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CF066123 OCSGQO9.y
CF066128 OCSGQO9.y
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BQ976411 QHIZ1J10.
BF3458 QVO-NN102
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NG2783 ye28102.81
AW797027 QV1-UM003
BI431277 949066E11
BX098115 BX098115
AW604870 QV1-CT036
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1MO005C08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0005C08 F, genomic survey sequence.
                                                  CE002581 tigr-g88-
AR893710 ARABAIGDB
AR803534 1M042120DB
AQ934191 RPCT-23-2
AA414435 VG08e10.8
B1082921 602878291
BB398492 BB398492
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                                     AV410806 AV410806
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                                                    CE002581
AX89310
AZ603534
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AA414435
BIO82921
BB198492
AQ545235
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CG559758
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BR466946
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BY082301
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AZ304985
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AUTHORS
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AZ304985 1M0005C08
CE086809 tigr-gss-
BG148573 uu84a06.y
BE009953 PM3-BN017
                                                                                       9, 2004, 02:50:24 ; Search time 2937.6 Seconds (without alignments) 975.888 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                               nucleic search, using sw model
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CE086809
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Gapop 10.0 , Gapext 1.0
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197
199
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seq length: 200
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26.7
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Perfect score:
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5

Result No.

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SOURCE
ORGANISM
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BG148573/c
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//done lib="Mouse lobb plasmid UUGCLM library"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (stratagene) cells
and selected for ampicillin resistance."
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The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. ( Úbasea; L. to 197) Trkness. E. F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUCAUAACC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GGAGAGGGTACCGGGTCATACTAATACTGCTACCCATTCTGCCATGCCCAGCACT 81
                                                                                                                                                                                                                                                                                                                                          lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.8%; Score 27.6; DB 28; Length 139; Best Local Similarity 54.5%; Pred. No. 2.1e+02; Matches 36; Conservative 6; Mismatches 24; Indels 0;
Smail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 139.
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CE086809/c
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T 3/1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Libra Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Farima Bonaldo."
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/clone="IMAGE:3382955"
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/lab_host="UmBE:3382955"
/note="Corgan: germinal B-cell; Vector: pT7T3D-Pac
/note: pT7T3D-Pac
/no
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UNB4a06.y1 Soares mouse NMGB bcell Mus musculus cDNA clone IMAGE:3382955 5' Similar to SW:PRI2_MOUSE P33610 DNA PRIMASE LARGE SUBNUT;' mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 199)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: egapbs.remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/clone_lib="Hog Library"
/noce="Site_l: BstXI; Libraries were prepared from
peripheral Blood"
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1 Similarity 50.0%; Pred. No. 3e+02;
40; Conservative 7; Mismatches 3
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Seg primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                              Location/Qualifiers
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76 TTCATTTCCCAGAGTTAGGT 57
                                                                                                                                         Email: ekirknes@tigr.org
Class: shotgun.
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Rockville, MD 20850,
                                             Tel: 301-838-0200
Fax: 301-838-0208
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Best Local Similarity
Matches 40; Conserv
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8 g ઠ

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1...175
/ Organism="Homo saptens"
/ Ab_axef="taxon:9606"
/ Clone="INAGE:316297"
/ Lissue_type="colon tumor, RER+"
/ Inb_host="DH10B"
/ Clone lib="NCI CGAP Col6"
/ Note="Gorgan: colon" Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plaemid DNA from the normalized library NGI CGAP Col0 was prepared, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144544-1143351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Grag Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

Location/Qualifiers
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                                                                                                                                                          BF000123 175 bp mRNA linear EST 06-OCT-2000 7h18b01.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:3316297 3' similar to TR:Q9W6S3 Q9W6S3 SAPK INTERACTING PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
  26
                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                          1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCCUCCCCAUUCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 CCGGGCAGTGCTCTCTCAATTCCAGCCTGCTTAACCCTGATCACTAT 133
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                                                                                                                                                                                                                                                                         BF000123.1 GI:10700398
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 175)
                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Best Local Similarity
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                                                                                                                 RESULT 5
BF000123
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AA168469
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KEYWORDS
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1 (hases 1 to 197)

Dias; Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpeon, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM3-BN0174-130 Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                      BE009953 197 bp mRNA linear EST 05-JUN-2000 PM3-BN0174-130500-007-d04 BN0174 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                  1 GGGAGAGGAAGAGGAGAGAGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG
                                                                                            Gaps
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                                               Length 199;
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                                             26.9%; Score 25.8; DB 12; 41.9%; Pred. No. 8.4e+02;
                                                                                          42;
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                                                                                                                                                                                                                            61 CUCAUAACCCAGAGGUCGAUAGUACUGGAUCCC 93
                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 56 High quality sequence stop: 197. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                          Conservative
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                                          Query Match
Best Local Similarity
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SOURCE
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BE009953/c
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VERSION
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AUTHORS
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ORIGIN
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Thermostabilization and thermoactivation of thermolabile enzymes by trehanostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayataw, N., Hori, P., Itohikwa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 161)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
20277479
10819328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AGAGAGGAAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGCUC
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Lotus japonicus young plants (two-week old) Lotus corniculatus var. japonicus cDNA clone WML078d06_r 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="stomach"
/dev_stage="adult"
/clone_lib="Mus musculus stomach C57BL/6J adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 24; DB 9; Length 159; 48.5%; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Indels
                                                                                                                                                                                                                                                                                             3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="2210418F19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                               Genome Science Laboratory RIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                    Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Conservative
                                                                                                                                                                                                                            Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   j. .159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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AV410806
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV081297 Aug musculus stomach C57BL/6J adult Mus musculus cDNA
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Mus musculus
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GATGAGGAATGTACTGCTTTGTTCATGCTGCCCCTACCAGGCCACTCCTACTCATGAGGA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 GAUGGGGACUADACCGCGUAAUGCUGCCUCCCAUUCCGGAACGCUCAUAACCCAGAGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                              The WashU-HIMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Nouse EST Project
WashU-HIMI Mouse EST Project
WashIngton University School of MedicineP
444 Forcet Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%; Score 25.2; DB 9;
44.9%; Pred. No. 1.3e+03;
iive 10; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28Ml3 rev2 from Amersham.
Location/Qualifiers
1..176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone 2210418F19, mRNA sequence.
AV081297
AV081297.1 GI:5212745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:10090"
/clone="IMAGE:598829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH108"
    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 CGAUAGUACUGGAUCCCC 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.99
Matches 35; Conservative
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                       ORGANISM
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Strizhov, N., Li, Y., Rosso, M. and Weisshaar, B.
Strizhov, N., Li, Y., Rosso, M. and Weisshaar, B.
Direct Submission
Submitted (15-DEC-2003) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene Atlg06940. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC16. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                   BX893710 117 bp DNA linear GSS 15-DEC-2003
Arabidopsis thaliana T-DNA flanking sequence GK-649H06-023273,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weisshaar, B.
                                102 GGGGGAGGAAATGGAAGGGGAGAGGGACAGTTTCAAGCAGACTCCCCACTAAGCACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 GGGAGGGGGCAGAGGCGCTGGGCGCAAACGTCCAAATGGGGCNTNCCAACCCAGTGCCT
       2 GGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGAGAGAGGAAGAGGGAUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG
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/mol type="genomic DNA"
/strain="Columbia 0"
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/clone="GK-649H06-023273"
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42 TCTCAAC 36
                                                                                                   62 UCAUAAC 68
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tigr-gss-dog-17000320893726 Dog Library Canis familiaris genomic,
genomic survey sequence.
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mkNA"
/isolate="Miyakojima MG-20"
/isolate="Miyakojima MG-20"
/db_xref="teaxon:34305"
/clone="MmL078d06_r"
/dev stage="young plants (two-week old)"
/clone_lib="Lotus japonicus young plants (two-week old)"
/note="vector: pBlueeriptil SK-; Site_1: EcoRl; Site_2:
Xhol; synonym: Lotus japonicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCAUUCCGGAACGCUCAUAACCCAGAGGUC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis. I (bases 1 to 200)
Xirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/note="Site 1: BstXI; Libraries were prepared
peripheral blood"
                                                                                                                               1. .lei
/organism="Lotus corniculatus var. japonicus"
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Pred. No. 3.6e+03;
4; Mismatches 27;
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/mol_type="genomic DNA"
/strain="Standard Poodle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CE002581.1 GI:34999116
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Best Local Similarity 53.7%;
Matches 36; Conservative 4
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Best Local Similarity 50.0%
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris
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CE Interest and the mouse BAC library RPCI-23. For BAC Clones are desired from the mouse BAC library RPCI-23. The grant Contact: Shaying Zhao St. Nerment of Enkaryotic Genomics Unpublished (1999)

Contact: Shaying Zhao Department of Enkaryotic Genomics Department of Enkaryotic Genomics Department of Enkaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 0200

Fax: 301 838 0200

Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterédejong.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@reegen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Sag primmer: 77
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/clone lib="RPCI-23"
/note="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site 2: ECORI; Female CS7BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                     GSS 21-DEC-1999
                               GGGAGAGAGGAAGGAGGAGGACUAUACCGCGUAAUGCUGCCUCCCCAUUCCGGAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                               AQ934191
RPCI-23-282P11.TV RPCI-23 Mus musculus genomic clone
RPCI-23-282P11, genomic survey sequence.
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/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-282P11"
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                                                                                                                                                                                                                                                                                 AQ934191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clon=[11b="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared bin high molar excess. The
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb| AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse sund annealed to
                                                                                                                                                                                                                                                                                                                                                                            SM Mus musculus
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 167)
I slam, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Context: Robert B. Weiss
University of Utah
Genome Center
                                                                                                                                                                                                 GSS 13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                         AZ603534 línear GSS 13-DEC-200
1M0422L20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0422L20 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0422 row: L column: 20
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 167.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"

/gtrain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIMO422L20"

/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                     AZ603534.1 GI:11725724
     75
CUCAUAACCCAGAGG
                                                   52 CTCACTATAGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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KEYWORDS
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73

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RESULT 13

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Gaps

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24.4%; Score 23.4; DB 28; Length 167; ilarity 49.2%; Pred. No. 4.7e+03; Conservative 7; Mismatches 26; Indels 0.

Query Match Best Local Similarity Matches 32; Conserv

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E (bases I to 167)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatau, N.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Korinara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Saro, K.,
Shibata, Y., Shigamoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Shigemoto, Y., Shinagawa, A.,
Matanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
Hayashizaki, Y.

Inpublished (2000)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB398492 RIKEN full-length enriched, ES cells Mus musculus CDNA clone C330008G22 3' similar to AF087680 Mus musculus valyl-tRNA BB398492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="tumor, biopsy sample"
/dev stage="5 months"
/lab_host="DH108"
/clone_lib="NCI COAP_Mam2"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11056 row: f column: 23
High quality sequence stop: 94.
Aammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                     1 (bases 1 to 190)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AGAGAGGAAGAGGGATTGTGTNTCTACAGCCTAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .190
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5009686"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="FVB/N-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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B1082921
B1082921.1 G1:14501251
EST.
                             AA414435 187 04-AUG-1997 vd08e10.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:791946 5' similar to TR:G1136422 G1136422 KIAA0181 PROTEIN ;,
                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 181)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HIMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.4%; Score 23.4; DB 9; Length 181; 55.1%; Pred. No. 4.8e+03; ive 6; Mismatches 16; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand Seq primer: -don13 Fwd. ET from Amersham High quality sequence stop: 178. Location/Qualifiers
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Matches 27; Conservative
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chenical Research (RIKEN)
Tel: Institute of Physical and Chenical Research (RIKEN)
Tel: 18145-503-2922
Email: genome-reseage: riken-go.jp/
Carninci.p. Nishlyama Y. Westrowr. A. Itoh, M., Nagaoka.S.,
Carninci.p. Nishlyama Y. Westrowr. A. Itoh, M., Nagaoka.S.,
Sasaki, M., Okazaki, Y. Wuramateu, M. and Haysahizaki, Y.
Thermograbilization and thermoactivation of thermolabile enzymes by
trahalose and its application for the synthesis of full length
cDM. Kiteunai, T. Akiyama J., Shibata, X., Izawa, M., Kawai, J.,
Tomatu, Y. Carninci, P., Shibata, Y., Ozawa, Y., Muramateu, M.,
Okazaki, Y. and Haysahizaki, Y. Ozawa, Y., Muramateu, M.,
Antomated filtration-based high-throughput plasmid preparation
system. Gone Res. old Shibata, Y., Ozawa, Y., Muramateu, M.,
Antomated filtration-based high-throughput plasmid preparation
system. Gone Res. old Shibata, Y., Ozawa, Y., Muramateu, M.,
Antomated filtration-based high-throughput plasmid preparation
system. Gone Res. old Shibata, Y., Ozawa, Y., Muramateu, M.,
Antomated filtration-based high-throughput plasmid preparation
system. Gone Res. old Shibata, Y., Ozawa, Y., Muramateu, M.,
Antomated filtration-based high-throughput plasmid preparation
system. Carninci, P. Shibata, Y., Ozawa, Y., Muramateu, M.,
Antomated filtration-based high-throughput plasmid preparation
system. Carninci, P., Shibata, Y., Ozawa, Y., Muramateu, J.,
Antomated filtration-based high-throughput plasmid preparation
system. Carninci, P., Shibata, Y., Ozawa, Y., Muramateu, J.,
Antomated filtration-based high-through one round of Bornel Science Laboratory was
propered by using trehalose thermo-activated reverse
proferon contributed to prepare mouse tissues. Ist strand conk of Schorel School Scho
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Query Match 24.2%; Score 23.2; DB 10; Length 167; Best Local Similarity 44.6%; Pred. No. 5.4e+03; Matches 41; Conservative 8; Mismatches 43; Indels 0; Gaps 0;

50 GGCAGGTGGATGAGGCCATCGCCCTTTTCCAGAAGATGCTGTGACCCCC

Search completed: April 9, 2004, 06:03:50 Job time : 2945.1 secs

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April 9, 2004, 01:42:24; Search time 283.067 Seconds (without alignments) 5206.064 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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is the number of results predicted by chance to have a Pred. No.

PAT 18-DEC-2003

linear

77 bp DN. Sequence 18123 from Patent EP1033401. AX902260

DEFINITION

VERSION

RESULT 1 AX902260 LOCUS

AX902260.1 GI:40057217 Homo sapiens (human)

sapiens

KEYWORDS SOURCE ORGANISM

ALIGNMENTS

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 18123 06-SEP-2000;

REFERENCE AUTHORS TITLE JOURNAL

ARA2268 Sequence BD11781 EST and e BD275880 COMPOUNDS AR220665 Sequence AR255659 Sequence AR281229 Sequence AR365924 Sequence AR365924 Sequence AR365924 Cell rece UZ6786 Mus musculu AU048750 Rattus no AJ048750 Rattus no AJ543147 Phaneroch L24891 Human chrom Ratolar D28372 Homo sapien M81089 Ambystoma m AF006569 Sus scrof AJ536093 Unculture AF509475 Bacterium AJ229270 Homo sapi AX913011 Sequence AF509475 Pan trogl AX913011 Sequence AF193475 Pan trogl AR28669 Sequence AK398959 Sequence AK202684 Sequence AK2086388 Mus muscu AF096318 Mus muscu AF096318 Human ret/P AR28957 Human ret/P AR58257 Musemophil X58257 Musemophil X5 AJ493433 Agrobacte AJ493434 Neisseria Z57295 H.sapiens C G26726 human STS S AY089788 Mus muscu AF012183 Mus muscu score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES AXO89787 AR173337 HAMADBL1 HSU32641 AF528054 MMMARK001 HUMUT452A CLI536093 F193462S03 AY013620 AF509475 HAJ9270 AX913011 BD048544 F193462S14 AR286969 AR398959 AX202684 ASP493433 NSP493434 HS170E10R G26726 S42430 MMU26786 AF096389 AF096378 AF096388 AY040741 HUMLBP31 AMTMHA2A AF006569 В Length 1113 127 189 94 141 141 159 38 38 38 78 78 161 16.8 16.2 17.22 17.22 17.22 17.22 17.22 17.22 17.22 17.23 Result No.

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BD275880.1 GI:33085648
JP 2002543769-A/274.
unidentified
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JP 2002010789-A/9898.
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1 (bases 1 to 77)

Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.

Saquence tag and encoded human protein

Patent: JP 2001269182-A 14039 02-OCT-2001;

GENSET
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JP 2001269182-A/14039
02-OCT-2001
04-PEB-2000 JP 2000118773
26-PEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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AR422268.1 GI:40177378
                                                                                                                                                                                                                                                                                     BD037793 77 bp DNA Sequence tag and encoded human protein. BD037793
                                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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    /organism="Homo sapiens"
/mol_type="genomic DNA"
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JP 2001269182-A/14039.
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 115)
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בשבי/בשט 196 bp DNA linear PAT 17-JUL-2003
COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER.
BD275880
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JP 2002010789-A/9898
15-JAN-2002
07-AQC-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
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Homo sapiens (human)
Homo sapiens
Homo sapiens
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 115)
Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
EST and encoded human protein
Patent: JP 2002010789-A 9898 15-JAN-2002;
GENSET CORP
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Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y..
EST's and encoded human proteins
Patent: US 6639063-A 13765 28-OCT-2003;
Location/Qualifiers
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/organism="Homo sapiens"
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/organism="unknown"
/mol_type="genomic DNA"
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BD117821
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PAT 10-APR-2003

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AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

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Wang, T., Wang, A., Skeiky, Y.A., Li,S.X., Kalos, M.D., Henderson, R.A., Mcneill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R., Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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UNCLOBESIFIED.
1 (bases 1 to 196)
1 (bases 1 to 196)
Wang, T., Fan, L., Kalos, M.D., Bangur, C.S., Hosken, N.A. and Fanger, G.R.
Compounds and methods for therapy and diagnosis of lung cancer Compounds and Si8256-A 317 11 FEB-2003;
Patent: US 6518256-A 317 11 FEB-2003;
Location/Qualifiers
                                      1 (bases 1 to 196)
Wang, T., Hosken, M.A., Kalos, M.D., Fanger, G.R. and Fan, L.
Compounds and methods for therapy and diagnosis of lung cancer
Patent: US 6482597-A 317 19-NOV-2002;
Location/Qualifiers
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AR201229
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CORIXA CORPORATION (US)
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Sequence 317 from Patent WO0200174.
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                     Unclassified.
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ISM unidentified unclassified.

Unclassified.

Example 1 (bases 1 to 196)

RS Wang,T. and Van,R.

COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER ALE PARENT: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER ALE PARENT: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER COTIXA CORPORTION et al.

COTIXA CORPORATION et al.

SS HOMO SEADIEN

PD 24-DEC-2002

PP 24-DEC-2002

PP 24-DEC-2002

PP 24-DEC-2002

PP 24-DEC-2002

PP 24-DEC-2002

PP 24-DEC-2002

PR 22-FEB-2000 US 09/510376,10-JAN-2000 US 09/480884, PR 02-APR-1999 US 09/466396

PI CONGROUP AND MAG, TIKN VAN

CC

FH KEY LONGLONG WANG, TIKN VAN

CC

FH KEY LOCATION/Qualifiers.
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Mang,Tr., Fan,Lr., Kalos,M.D., Bangur,C.S., Hosken,N.A., Fanger,G.R.,
Li,S.X., Wang,A., Skeiky,Y.A.W., Henderson,R.A. and McNeill,P.D.
Compositions and methods for the therapy and diagnosis of lung
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So.6%; Score 17.2; DB 6; Length 196;
Best Local Similarity 56.7%; Pred. No. 8.2e+04;
Matches 17; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 17.2; DB 6; Length 196; 56.7%; Pred. No. 8.2e+04; ive 5; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/mol_type="genomic DNA"
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Best Local Similarity 56.7
Matches 17; Conservative
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DEFINITION

RESULT 6 AR220665

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ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

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Gaps

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PAT 15-FEB-2002

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KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 7 AR255659

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ACCESSION VERSION

ORIGIN

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 135)
De Palma,R., Del Galdo,F., Milan,G. and Bronte,V.
Analysis of T cell receptor repertoire of CTL recognizing the mouse melanocyte differentiation antigen TRP-2
                       Mus musculus T cell receptor Va5/Ja36 alpha chain mRNA, isolate U26786
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Mus musculus TRP-2 specific T-cell receptor AV5 mRNA, partial cds.
AY089788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-MAY-1995) Fei F. Shih, The Wistar Institute of Anatomy and Chemistry, 3601 Spruce Street, Philadelphia, PA 19104,
                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 123)
Shih,F.F., Cerasoli,D.M. and Caton,A.J.
A major T cell determinant from the influenza virus hemagglutinin (HA) can be a cryptic self peptide in HA transgenic mice
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Direct Submission
Submitted (13-MAR-2002) Clinical and Experimental Medicine, University of Naples, S. Pansini 5, Naples 80131, Italy 1..135
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/cell_type="T-helper cell, hybridoma"
<1. .>123

    .123
    /organism="Mus musculus"

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/strain="BALB/c"
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Casanova, J.L., Cerottini, J.C., Matthes, M., Necker, A., Gournier, H., Barra, C., Widmann, C., MacDonald, H.R., Lemonnier, F., Malissen, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           et,al.
H-2-restricted cytolytic T lymphocytes specific for HLA display T
eceptors of limited diversity
J. Exp. Med. 176 (2), 439-447 (1992)
92364546
                                                                                                                                                                                                                                                                                                                                                                                                                                                        S42430

T cell receptor alpha chain, T cell receptor alpha chain { nonproductive rearrangement } { mice, HLA-Cw3-reactive CTL clone CV3/1.1, Genomic, 104 nt].
S42430
S42430.1 GI:253590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created this entry [NCBI glabbg 111091] from the original journal article. This sequence comes from Fig. 3B.

Location/Qualifiers
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                                                                                            Query Match 50.6%; Score 17.2; DB 6; Length 196; Best Local Similarity 56.7%; Pred. No. 8.2e+04; Matches 17; Conservative 5; Mismatches 8; Indels
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/note="This sequence comes from Fig. 38"
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/product="T_cell_receptor_alpha_chain"
/protein_id="AAB61953.1"
/b_refe="G1:253591"
/translation="HPGDSAAYFCAVKILEEAMQS"
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protein id="AAB63954.1"
db_xref="GI:253592"
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/gene="T cell receptor alpha chain"
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                                                                                                                                                                                                                                                                       104 GGAGATTGGACGCCTGATGCTCCCTCCCC 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus sp."
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REFERENCE AUTHORS

RESULT 10

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176 bp DNA linear STS 20-JAN-2000 OTSUKA clone, 765all, microsatellite sequence,
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Phanerochaete chrysosporium partial mRNA for putative Hsp70 protein
AJ543747
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hsp70 gene; Hsp70 protein.
Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)
Phanerochaete chrysosporium
Phanerochaete chrysosporium
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
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Watanabe, T.K., Hishigaki, H., Okuno, S., Mizoguchi, A., Oga, K., Tsuji, A., Ono, T., Yamasaki, Y., Kanemoto, N., Takahashi, E., Irie, Y., Takamura, Y., Takagi, Y. and Tanigami, A. The large-scale mapping of rat microsatellite markers
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research
Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno,
Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan
(E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,
Fax:+81-886-37-1035)
                                                                                                             Gaps
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                                                                        Score 17; DB 10; Length 157;
Pred. No. 1.1e+05;
5; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="liver"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
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 153. .157
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                                                                        50.0%;
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AU048750
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                                                                                                                                                                                                                                                                                                   Rattus norvegicus,
                                                                                          Best Local Similarity 60.0
Matches 15; Conservative
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                                                                          Query Match
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AU048750
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Submitted (02-JUL-1997) Fels Institute for Cancer Research and
Molecular Biology, Temple University School of Medicine, 3420 North
Broad Street, Philadelphia, PA 19140, USA
Location/Qualifiers
                                                                                                                         /codon_start=1
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R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF012183
Mus musculus T-cell receptor alpha chain (TCRA) mRNA, partial cds.
AF012183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus bularzoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mauzayota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 157)
Lin, W.L., Kuzmak, J., Pappas, J., Peng, G., Chernajovsky, Y., Palasoucas, C.D. and Oleszak, E.L.
Amplification of T-cell receptor alpha- and beta-chain transcripts adaptor-polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 157)
Lin, W.L., Kuzmak, J., Pappas, J., Chernajovsky, Y., Platsoucas, C.D.
and Oleszak, E.L.
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                                                                                                                                                                                                                                                                                Length 135;
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103. .152
                                                                                        <1. . . > 135
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/gene="TCRA"
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Best Local Similarity 60.0%;
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                                                                                        CDS
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Location/Qualifiers

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| Mol_type="mRNA"
| Mol_type="mRNA"
| Mol_type="mRNA"
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| Moletaxon:5306"
| Moletaxon:530708"
| Moletaxon:530708"
| Moletaxon:540108**
| Moletaxon:54010**

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                                                                                      Assmann, E.M.
Iron-responsive genes in Phanerochaete chrysosporium
Upublished
(Dases 1 to 186)
Assmann, E.M.
Birect Submission
Submitted (10-FEB-2003) Assmann E.M., Chmeg, Universidade Estadual
de Campinas, Caixa Postal 6010, Campinas, Sao Paulo, 13093-020,
BRAZIL
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Aphyllophorales; Corticiaceae; Phanerochaete.
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Search completed: April 9, 2004, 03:53:27 Job time: 286.067 secs

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Compugen Ltd.		Search time 120.8 Seconds (without alignments)
Copyright (c) 1993 - 2004 Compugen Ltd.	- nucleic search, using sw model	April 9, 2004, 01:39:24 ; Search time 120.8 Seconds (without alignments)

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Run on:

GenCore version 5.1.6

1195.685 Million cell updates/sec			tengececan 34
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	Title:	core:	מפלות פוזרם:

3373863 segs, 2124099041 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

3774412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* N_Geneseq_29Jan04:* geneseqn2001as:* geneseqn2001bs:* geneseqn2004s:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn20028:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	QI	ABN88557	ABZ21241	ABZ21259	ABZ21242	ABN88490	ABZ21269	AAC14048	ACD79614	AAC66013	ABL49232	ABQ92418	ADA28407	ABZ21265	ABZ21277	ABZ21266	ABZ21260	AAT43544	AAI24741	ABA70029	AAI50142	ABA36840	AAK44134	AAK18238
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مد	Match	100.0	100.0	100.0	100.0	100.0	61.8	50.6	50.6	50.6	50.6	50.6	50.6	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
	Score	34	34	34	34	34	21	17.2	17.2	17.2	17.2	17.2	17.2	17	17	17	17	17	17	17	17	17	17	17
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24 17 50.0 112 4 ABS43790 25 16.2 47.6 113 4 ARAG5564 27 16.2 47.6 113 4 AAK47625 28 16.2 47.6 113 4 AAK47625 30 15.8 46.5 51 4 AAK77108 31 15.6 45.9 31 7 ABZ21284 32 15.6 45.9 31 7 ABZ2128 34 15.6 45.9 76 4 AAK4728 35 15.6 45.9 76 4 AAK4728 36 15.6 45.9 164 4 AAK4728 37 15.6 45.9 164 4 AAK4728 38 15.6 45.9 164 4 AAK4728 40 15.6 45.9 164 4 AAK4728 41 15.6 45.9 164 4 AAK4728 42 15.6 45.9 164 4 ABA31461 43 15.6 45.9 164 4 AAK4728 44 15.6 45.9 164 4 AAK4728 45 15.6 45.9 164 4 ABA31461 46 15.6 45.9 164 4 ABA31461 47 15.6 45.9 164 4 ABA31461 48 15.6 45.9 164 4 ABA31461 49 15.6 45.9 164 4 ABA31461 41 15.6 45.9 164 4 ABA31461 42 15.6 45.9 164 4 ABA31461 43 15.6 45.9 164 4 ABA31821 44 15.6 45.9 164 4 ABA31821	Abs43790 Human liv	Abs18369 Human gen	Aba69564 Human foe	Aak43625 Human bon	Aak17785 Human bra	Aak67210 Human imm	Aal31035 Human SNP	Abz21244 FIXa apta	Abz21258 Aptamer 9	Aas48228 Enterococ	Aca12905 Prokaryot	Aac24799 Human sec	Abg90618 M. capsul	Aai21015 Probe #10	Aba66087 Human foe	Aai46268 Probe #14	Aba48207 Human bre	Aba33163 Probe #11	Aak40252 Human bon		Abs39826 Human liv	Aai06732 Probe #67
10.00 10	ABS43790	ABS18369	ABA69564	AAK43625	AAK17785	AAK67210	AAL31035	ABZ21244	ABZ21258	AAS48228	ACA12905	AAC24799	ABQ90618	AA121015	ABA66087	AA146268	ABA48207	ABA33163	AAK40252	AAK14510	ABS39826	AAI06732
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	20.0	50.0	47.6	47.6	47.6	47.6	46.5	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9
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ALIGNMENTS

RESULT 1

Coagulation factor IXa (FIXa) aptamer SEQ ID NO:70. ВР. ABN88557 standard; RNA; 34 (first entry) 19-AUG-2002 ABN88557; ABN88557

RNA aptamer; identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis;

26-SEP-2001; 2001WO-US030004. bypass graft surgery; ss WO200226932-A2. Homo sapiens. 04-APR-2002. Synthetic.

26-SEP-2000; 2000US-0235654P CP; Sullenger BA, Rusconi WPI; 2002-479560/51. (UYDU-) UNIV DUKE.

Novel RNA aptamers that selectively bind coagulation pathway factors, E2 family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.

Claim 14; Page 25; 216pp; English.

The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoietin-1 (Angi) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have cardiant and cyrostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

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/note= "All purines are 2'hydroxyl and pyrimidines are 2'
biological activity of the coagulation pathway factor in the warm-
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inflammatory proliferative disease; hypoglycaemia; human;
coagulation Factor IXa; FIXa; ss.
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/bound_moiety= "Nucleotides 1.
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/mod_base= OTHER
/not== "idT"
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07-NOV-2001; 2001US-0331037P.
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                                                                                                                                                              Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
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inflammatory proliferative disease; hypoglycaemia; ss.
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/bound moiety= "Nucleotides 28.
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/note= "mg mU mC
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                                                       Rusconi C;
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25-MAY-2001; 2001US-0293231P.

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The present invention relates to a method for altering the affinity of a nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient or in vitro, or reversing the binding of the labelled ligand to a target tissue. The method comprises administering a medulator that binds to the ligand to a patient receiving the ligand, or contacting the ligand with the modulator under conditions such that the modulator binds to the ligand, and thus alters the affinity of the ligand for the target molecule. The method is useful for treating a number of disorders e.g. infection, autoimmunity, tumours, inflammatory proliferative diseases and
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                                                                                                                                                                                                                                                                                                                                                         hypoglycaemia. The present sequence is an aptamer to human coagulation
Factor IXa (FIXa aptamer), which was used to illustrate the method of the
                                                                                            Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
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                               Rusconi C;
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                                                               WPI; 2003-140438/13.
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Best Local Similarity
 (UYDU-) UNIV DUKE.
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                                                                                                                          Altering affinity of nucleic acid ligands for target molecules in a. patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
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07-NOV-2001; 2001US-0331037P
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                                                              Rusconi
                                                                                            WPI; 2003-140438/13.
                              (UYDU-) UNIV DUKE.
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WPI; 2003-140438/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes RNA aptamers (I,II) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angloopietin-I (Angl) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-coagulation activity of the coagulation pathway factor in the warm-blooded vertebrate (I) are useful for modulating E2F cardiovascular diseases in the mammal. (II) are useful for modulating E2F cardiovascular diseases in the mammal. (II) are useful for modulating E2F cardiovascular and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for modulating angiogenesis. The RNA aptamers are also useful for diagnostic modulating angiogenesis. The RNA aptamers are useful as diagnostic creagents to detect the presence or absence of target substances to which they complicially bind, and for identifying substances to which they specifically bind. Ann88488 to absence of targets to which they specifically bind. Ann88488 to Anna to a respect to which they was sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIXa aptamer 9.3t&9.3t-3NT oligonucleotide modulator, AS 5-1, SEQ ID 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mod_base= OTHER
/note= "All nucleotides are 2'Omethyl oligonucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 34; DB 6; Length 96; 100.0%; Pred. No. 8.1e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunosuppressive, aptamer, infection, autoimmunity, tumoi
inflammatory proliferative disease, hypoglycaemia, human,
coagulation Factor IXa, FIXa, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 96 BP; 24 A; 27 C; 29 G; 0 T; 16 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
Claim 13; Fig 1A; 216pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001; 2001US-0293231P. 07-NOV-2001; 2001US-0331037P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-2002; 2002WO-US016555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ21269 standard; RNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 34; Conservative
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*tag≃
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ21269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The present invention relates to a method for altering the affinity of a nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient or in vitro, or reversing the binding of the labelled ligand to a target tissue. The method comprises administering a modulator that binds to the ligand to a patient receiving the ligand, or contacting the ligand with the modulator under conditions such that the modulator binds to the ligand, and thus alters the affinity of the ligand for the target molecule. The method is useful for treating a number of disorders e.g. infection, autoimmunity, tumours, inflammatory proliferative diseases and hypodyvaemia. The present sequence is an oligonouteotide modulator, which targets the FIXa aptamers 9.3t and 9.3t-3NT. The FIXa aptamers bind to human coagulation Factor IXa and were used to illustrate the method of the invention. This oligonoutleotide was found to be effective at reversing FIXa aptamer's anticoagulation activity in human plasma in
Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numan; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7; Length 23; 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 5 A; 7 C; 5 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 18123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 7
Pred. No. 6.4;
4; Mismatches
                                                                                                                                                                                          Claim 50; Page 74; 111pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.8%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC14048 standard; cDNA; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 81.0°
Matches 17; Conservative
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identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
   mRNAs encoding secreted proteins. No ORF has yet been conclusively
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 77 BP; 31 A; 16 C; 14 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                              expression and secretion vectors
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ö Gaps ; 0 DB 3; Length 77; Indels Score 17.2; DB 3; Pred. No. 4.5e+02; 5; Mismatches 2 UGGGGACUAUACCGCGUAAUGCUGCCUCCC 31 + TGGGAACTATGTCAGGAAAACCTGCCTCCC 33 50.6%; 17; Conservative Query Match Best Local Similarity Best Loca Matches ઠે 셤

AAC66013 standard; cDNA; 196

RESULT 9

(first entry)

21-FEB-2001

AAC66013;

E. coli K12 MG1655 biochip probe SEQ ID 10890. ACD79614/c ID ACD79614 standard; DNA; 100 BP. 19-SEP-2003 ACD79614; RESULT 8

Biochip; gene expression; gut; diagnostic; detection; probe; ss. Escherichia coli. EP1260592-A1 27-NOV-2002

(MWGB-) MWG-BIOTECH AG.

17-MAY-2001; 2001EP-00112179. 17-MAY-2001; 2001EP-00112179.

Huber A, Donner H, Drescher B,

WPI; 2003-241155/24.

Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expression patterns.

Claim 3; Page 1697; 2004pp; German.

This invention describes a novel blochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least cone includes a segment of at least 20 bases identical with or complementary to, a segment of an least 20 bases identical with or complementary to, a segment of an open reading frame (orf) of Escherichia (orl K12 and for determining the gene expression pattern, e.g. for in X12 and for determining the gene expression pattern, e.g. for diagnostic determine the effects of e.g. growth media on gene expression. The blochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows

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measurements of population densities for the various strains. The use of synthetic oligonuclectides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD81540 represent oligonucleotide probes used with the biochip described
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                              Length 100;
                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                       Sequence 100 BP; 23 A; 21 C; 31 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                            Score 17.2; DB 7;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                1 AUGGGGACUAUACCGCGUAAUGCUGCCUCC 30
                                                                                                                                                                                                                                                                                                                                       82 Argeccarcaarceceraareceeerre 53
                                                                                                                                                                                                              50.6%;
                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 18; Conservative
                                                                                                                             in the invention
                                                                                                                                                                                                            Query Match
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cancer; therapy; treatment; human; tumor; immunogenic; cytostatic; Human lung cancer-associated cDNA clone 25331. 99US-00285479. 99US-00466396. 99US-00476496. 03-APR-2000; 2000WO-US008896 10-JAN-2000; 2000US-00480884 22-FEB-2000; 2000US-00510376 vaccine; detection; ss. (CORI-) CORIXA CORP. WPI; 2000-628399/60 Fan L; WO200061612-A2. Homo sapiens. 02-APR-1999; 17-DEC-1999; 30-DEC-1999; 19-OCT-2000 Wang T, Lung

comprising an immunogenic portion of a lung tumor protein or variant (P2) which have eytoetatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention dan be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient ear treated with P2, polynucleotides encoding P2 or antigen presenting development of cancer. Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer This invention describes a novel isolated polypeptide (I) which Claim la; Page 233; 261pp; English. in a patient.

Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;

Length 196; DB 3; 50.6%; Score 17.2;

Query Match

ABL49232

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The present invention describes isolated human lung carcinoma polymucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polymucleotide that hybridises to the oligonucleotide and comparing the amount of polymucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaccutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABO22145 to ABO22486 and ABPG1866 to ABPG1952 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
                                                                                                                                                                                           Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine; gene;
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Pred. No. 5.4e+02;
5; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson
Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR,
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                            Human lung cancer associated cDNA sequence SEQ ID NO:317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 317; 381pp; English.
    ABQ92418 standard; cDNA; 196 BP.
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28-JUN-2001; 2001US-00897778.
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Best Local Similarity 56.7%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-583465/62.
                                                                                                                                                                                                                                                                                                               WO200247534-A2.
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                             07-OCT-2002
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                                                   AB092418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes human lung tumour proteins. Human lung activaties, and can be used in vaccine production. Compositions comprising the lung tumour proteins, proteins, proteins, proteins, polynucleotides, antibodies, proteins, proteins, proteins, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL49359 to ABL49300 and ABB77946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henderson
                                                                                                                                                                                                                                                                                                                                                                                    Human lung tumour cDNA sequence clone 25331 SEQ ID NO:317.
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD,
Mcneill PD, Fanger N, Retter MW, Marnerakis M,
Vedvick TS, Carter D, Watanabe Y, Peckham DW;
                        8
    56.7%; Pred. No. 5.4e+02;
                                                                                                  104 GGAGATTGGACGCCTGATGCTCCCTCCCC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 GGAGATTGGACGCCTGATGCTCCCTCCCC 133
                           5; Mismatches
                                                                       32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 309-310; 374pp; English.
                                                                       GGGGACUAUACCGCGUAAUGCUGCCUCCCC
                                                                                                                                                                                                                                          ABL49232 standard; cDNA; 196 BP
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21-AUG-2000; 2000US-00643597.
15-SEP-2000; 2000US-00662786.
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12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2000; 2000US-00606421
Best Local Similarity 56.79
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         response; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200174-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                     01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002
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Vedvick TS;

Henderson RA

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Gaps

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RESULT 11 ABQ92418

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The present invention relates to a method for altering the affinity of a nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient or in vitro, or reversing the binding of the labelled ligand to a target tissue. The method comprises administering a modulator that binds to the ligand to a patient receiving the ligand, or contacting the ligand with the modulator under conditions such that the modulator binds to the ligand, and thus alters the affinity of the ligand for the target molecule. The method is useful for treating a number of diseases e.g. inflection, autoimmunity, tumours, inflammatory proliferative diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypoglycaemia. The present sequence is an oligonucleotide modulator, which targets FIXa aptamer 9.3t. FIXa aptamer binds to human coagulation
                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "All nucleotides are 2'Omethyl oligonucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor IXa and was used to illustrate the method of the invention
                                                                                                                                               Immunosuppressive, aptamer, infection, autoimmunity, tumoi
inflammatory proliferative disease; hypoglycaemia, human;
coagulation Factor IXa; FIXa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 17; DB 7; Length 17; 70.6%; Pred. No. 4.3e+02;
                                                                                                         FIXa aptamer 9.3t oligonucleotide modulator, SEQ ID 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-2002; 2002WO-US016555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2001; 2001US-0293231P.
07-NOV-2001; 2001US-0331037P.
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17 TAATGCTGCCTCCCAT
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/*tag= a
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                                                                16-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                              WO200296926-A1.
                                                                                                                                                                                                                                                                                Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sullenger BA,
                                                                                                                                                                                                                                      Unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to ligand
                      ABZ21265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; at sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This sequence represents a human lung tumour cDNA isolated from a lung squamous cell carcinoma that may be useful in the diagnosis and treatment of lung cancer and other disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ' YAW, Li SX, Kalos MD, Henderson RA;
Retter MW, Durham M, Fanger GR, Vedvick TS;
Peckham DW, Cai F, Foy TM;
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Pred. No. 5.4e+02;
5; Mismatches 8; Indels (
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                                        gene therapy; vaccine; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 GGAGATTGGACGCCTGATGCTCCCTCCC 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 224; 296pp; English
Human lung tumour DNA clone 25331
                                   cancer; lung cancer; gene therap:
lung squamous cell carcinoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-00542615.
2000US-00606421.
2000US-00630940.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-00643597
2000US-00662786
                                                                                                                                                                                                                                    30-NOV-2001; 2001US-00007700
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99US-00476496
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Best Local Similarity 56.7%;
Matches 17; Conservative
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Carter D, Watanabe Y,
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                                                                                                                                               US2003064947-A1.
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02-AUG-2000;
21-AUG-2000;
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10-JAN-2000;
                                                                                                      Homo sapiens
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Wang T,

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Gaps

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16-APR-2003 (first entry)

RESULT 13 ABZ21265/c ID ABZ21265 standard; RNA; 17 BP.

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Location/Qualifiers

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Key
modified base
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                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for altering the affinity of a nucleic acid ligand (e.g. an appeamer) for a target molecule in a patient or in vitro, or reversing the binding of the labelled ligand to a target tissue. The method comprises administering a modulator that binds to the ligand to a patient receiving the ligand, or contacting the ligand with the modulator under conditions such that the modulator binds to the ligand, and thus alters the affinity of the ligand for the target molecule. The method is useful for treating a number of disorders e.g. infection, autoimmunity, tumours, inflammantary proliferative diseases and bypoglycaemia. The present sequence is an oligonucleotide modulator, which targets the FIXa aptamers 9.3t and 9.3t.3NT. The FIXA aptamers bind to human coagulation Pactor IXa and were used to illustrate the method of the invention. This oligonucleotide was found to be effective at
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                                                                                                                                                                                                                                                                                              Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
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                       Immunosuppressive; aptamer; infection; autoimmunity; tumour;
inflammatory proliferative disease; hypoglycaemia; human;
coagulation Factor IXa; FIXa; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 7; Length 17; Pred. No. 4.3e+02; 3; Mismatches 0; Indels
FIXa aptamer oligonucleotide modulator, 5-2C, SEQ ID 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              Claim 50; Page 75; 111pp; English.
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                                                                                                                                                       28-MAY-2002; 2002WO-US016555
                                                                                                                                                                                 25-MAY-2001; 2001US-0293231P, 07-NOV-2001; 2001US-0331037P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 50.0%;
Local Similarity 82.4%;
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AUGGGGACUAUACCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                              Sullenger BA, Rusconi C;
                                                                                                                                                                                                                                                                       WPI; 2003-140438/13.
                                                                                                                                                                                                                      (UYDU-) UNIV DUKE
                                                                                                     WO200296926-A1
                                                                             Unidentified.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
                                                          /note= "All nucleotides are 2'Omethyl oligonucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 50; Page 74; 111pp; English.
                           OTHER
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70.6%;
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07-NOV-2001; 2001US-0331037P.
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Sequence 26, Appl
Sequence 65, Appl
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Sequence 65, Appl
Sequence 126, Appl
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APPLICANT: Rails, long-ong
APPLICANT: Rails, Michael D.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Booken, Mancy
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Manchil, Parricia D.
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION HUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 115;
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APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS.
FILE REPERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11765
US-08-479-724A-12
US-08-479-724A-12
US-08-92-793-12
US-09-849-928-12
US-09-849-928-12
US-09-849-928-12
US-09-621-976-18097
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US-09-621-976-13765
; Sequence 13765, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
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Patent No. 6426072
GENERAL INFORMATION:
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Wancy
Fanger, Gary R.
Li, Samuel X.
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Best Local Similarity 56.7%;
Matches 17; Conservative
   ORGANISM: Homo sapiens
US-09-621-976-13765
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US-09-643-597-317

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134, App
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2661, Ap
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6423, Ap
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Sequence 317, App
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Sequence 6, Appli
Sequence 1341, Ap
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                                                                                                                           April 9, 2004, 02:54:20 ; Search time 27.8667 Seconds (without alignments) 677.093 Million cell updates/sec
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Sequence 18, P
Sequence 2661,
Sequence 1721,
Sequence 1341,
Sequence 6, Ap
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.: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-540-615A-317

US-09-606-615A-317

US-08-448-267A-6

US-09-474-432B-1341

US-09-474-432B-1341

US-09-134-001C-282

US-09-134-001C-282

US-09-134-001C-282

US-09-134-001C-282

US-09-136-0486-241-1

US-08-585-593A-18

US-08-56-171E-2661

US-08-56-171E-2661

US-08-56-171E-2661

US-08-61-77-530-6

US-08-477-530-6

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US-08-472-255A-12
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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34
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Match Length
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APPLICANT: Hosken, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45568
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
SUMBER OF SEQ ID NOS: 350
SOFTWARE: FASTERE for Windows Version 3.0
SEQ ID NO 317
LENGTH: 196
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HOSKEL, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
NUMBER OF ED ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 84;
5; Mismatches
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                                                                                                                                                                                                           3 GGGGACUAUACCGCGUAAUGCUGCCUCCCC 32
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                              Sequence 317, Application US/09480884A Patent No. 6482597 GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-542-615A-317
; Sequence 317, Application US/09542615A
; Patent No. 6518256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy A.
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Best Local Similarity 56.7%;
Matches 17; Conservative
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Best Local Similarity 56.77
Matches 17; Conservative
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Fan, Liqun
                                                                   ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-317
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CRGANISM: Homo sapien
US-09-480-884A-317
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; ORGANISM: Homo sapien
US-09-542-615A-317
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APPLICANT: Wang, T
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LENGTH: 196
                  SOFTWARE: FA
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Patent No. 592558
GENERAL INFORMATION:
APPLICANT: Earle, Steven R.
APPLICANT: Jacobson, Walter E.
TITLE OF INVENTION: Nucleic Acid Primers for Amplification
TITLE OF INVENTION: of a Mycobacteria RNA Template
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5925518el Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BANGE, CLAILED S.
APPLICANT: BANGE, MANCY
APPLICANT: Hosken, Mancy
APPLICANT: Hosken, Mancy
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: MANG, AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFRENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
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1300 Piccard Drive, Suite 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.2; DB; Pred. No. 84; 5; Mismatches
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Query Match 50.6%; Score 17.2; D
Best Local Similarity 56.7%; Pred. No. 84;
Matches 17; Conservative 5; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,267A
FILLING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Gormley, Mary E.
                                                                                                                                                                                                                                                              Sequence 317, Application US/09606421B Patent No. 6531315
                                                                                                                                                                                                                                                                                                                                                                          Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.7°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-606-421B-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 Pic
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APPLICANT: Religalman, Leo
APPLICANT: Religalman, Leo
APPLICANT: Belgalman, Leo
APPLICANT: Belgalman, Leo
APPLICANT: Belgalman, Leo
APPLICANT: Belgalman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Sweedler, Dave
APPLICANT: Sweedler, Dave
APPLICANT: Sweedler, Dave
APPLICANT: Shawn
TITLE OF Innen, Shawn
TITLE OF INNENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleor
FILE REFERENCE: MBHB00-831-C (249/073)
CURRENT APPLICATION NUMBER: 09/476,387
CURRENT FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-4-28
PRIOR PILING DATE: 1999-10-4-28
PRIOR PILING DATE: 1999-10-4-28
PRIOR PILING DATE: 1999-10-6-3
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 1524
NUMBER OF SEQ ID NOS: 1524
CONTAMER: PatentIn Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-476-387-1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shen, Che-Kun James
TITLE OF INVENTION: HS-40 ENHANCER-CONTAINING VECTOR
FILE REFERENCE: 08919/016001
CURRENT APPLICATION NUMBER: US/09/536,094
CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 09/205,015
PRIOR FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 45.3%; Score 15.4; DB 4; Best Local Similarity 51.5%; Pred. No. 4e+02; Matches 17; Conservative 5; Mismatches 11;
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45.3%; Score 15.4; DB 4;
Best Local Similarity 45.5%; Pred. No. 5.2e+02;
Matches 15; Conservative 7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
                33 TGGAGACCTTGACTCGCCTTTCGGCCTCCCCAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 TGGAGACCTTGACTCGCCTTTCGGCCTCCCCAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                   RESULT 8
US-09-476-387-1340/c
; Sequence 1340, Application US/09476387
; Patent No. 6617438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09536094 Patent No. 6303845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-536-094-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 147
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APPLICANT: Beaudry, Amber
APPLICANT: Beaudry, Andex
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenda
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-474-432B-1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 5..21
OTHER INFORMATION: /note= "T7 RNA polymerase promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 2; Length 46;
Pred. No. 77;
5; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: 25..46
; OTHER INFORMATION: /note= "hybridization region"
US-08-448-267A-6
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45.3%; Score 15.4; DB 4;
Best Local Similarity 51.5%; Pred. No. 4e+02;
Matches 17; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA primer"
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR PILING DATE: 1997-11-05
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-11-04
PRIOR PILING DATE: 1999-11-04
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SSOFIWARE: Patentin version 3.0
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 ACTATAGGGAGAACTGCTGCCTCCC 40
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; Sequence 1341, Application US/09474432B
; Patent No. 6528640
REGISTRATION NUMBER: 34,409
TELECOMUNICATION INFORMATION:
TELEPHONE: 301.258-5200
TELEFAX: 301.977-0847
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANBDENESS: single
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Best Local Similarity 60.0%;
Matches 15; ;Conservative !
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Sequence 18, Application US/08585593A

Patent No. 6503706

GENERAL INFORMATION:
APPLICANT: ABBEN, Hinrich J
APPLICANT: ANGER, Herbert
ITILE OF INVENTION: METHOD OF IDENTIFYING HUMAN AND ANIMAL
TITLE OF INVENTION: CELLS CAPALE OF UNLIMITED PROLIFERATION OR TUMOR
TITLE OF INVENTION: FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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sequence 1, Application US/09486241
patent No. 6472184
GENERAL INFORMATION:
APPLICANT: Hegement Peter
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEIC ACID
TITLE OF INVENTION: POLYMERS
FILE REFERENCE: 3910/66706
CURRENT APPLICATION NUMBER: US/09/486,241
CURRENT FILING DATE: 2000-02-22
PRIOR FILING DATE: 1996-08-17
PRIOR FILING DATE: 1997-08-17
PRIOR FILING DATE: 1997-08-17
PRIOR FILING DATE: 1997-08-17
SEQ ID NO:
SEQ ID NO:
LENGTH: 46
LENGTH: 46
LENGTH: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,593A
FLING DATE: 13-JUL-1996
PRIOR APPLICATION NUMBER: PCT/EP94/02307
FILING DATE: 13-JUL-1994
PRIOR APPLICATION NUMBER: DE P 43 23 727.4
FLING DATE: LS-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.5%; Score 14.8; DB 4;
55.9%; Pred. No. 7.8e+02;
tive 3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
TELECOMMUNICATION:
TELEPHONE: (202)638-S000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.9°
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Primer US-09-486-241-1
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STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Parent No. 6476212
GRNERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVERTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR TILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 6423
LENGTH: 117
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45.3%; Score 15.4; DB 4; Length 183;
Best Local Similarity 56.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 5; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 44.1%; Score 15; DB 4; Length 117; Similarity 50.0%; Pred. No. 7.6e+02; 16; Conservative 5; Mismatches 11; Indels
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OTHER INFORMATION: Incyte ID No. 6476212 700351779H1
                                                           104 IGCTGATTACAACCTCTGGTGCTGCTCCCCCT 136
                     2 UGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GGGTCCATACGGCGTTGTTCTGGANTCCCGT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ACUAUACCGCGUAAUGCUGCCUCCC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA; ORGANISM: Staphylococcus epidermidis US-09-134-001C-282
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Best Local Similarity
Matches 16; Conserva
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ORGANISM: Zea mays
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LOCATION: 31
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US-09-134-001C-282/c
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US-09-313-294A-6423
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US-09-486-241-1/c
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12 ATGGGGTAATTTCCGCCAAATCCCGTTTCCCCCT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craig A. Rosen
Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
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43.5%; Score 14.8; DB 4; Length 130;
Best Local Similarity 50.0%; Pred. No. 9.6e+02;
Matches 17; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                    Score 14.8; DB 4; Length 94;
Pred. No. 9e+02;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR DATE: 20-Oct-1997
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 88/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 2661: US-08-956-171E-2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-956-171E-2661
; Sequence 2661, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; APPLICANT: Charles Application
                                                                                                                                                                                                                                                               5 GGACUAUACCGCGUAAUGCUGCCUCC 30
                                                                                                                                                                                                                                                                                        52 GGGCTGCACAGAAATCCTGCCTCC 77
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TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2661:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                        Query Match
Best Local Similarity 57.7%;
Matches 15; Conservative
                  LENGTH: 94 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: DNA
SEQUENCE CHARACTERISTICS LENGTH: 94 base pairs
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1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCAU 34

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthesized nucleic acid molecule US-09-168-947-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.6; DB 4;
Pred. No. 9.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
42.9%; Score 14.6; I
Best Local Similarity 55.2%; Pred. No. 9.86
Matches 16; Conservative 4; Mismatches
                                                                                                                                    CENERAL INCORPORTATION:
APPLICANT: KACIALLY, DANIEL L.
APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
CURRENT APPLICATION NUMBER: US/09/168,947
CURRENT FILING DATE: 1998-10-08
EARLIER FILING DATE: 1995-66-06
EARLIER FILING DATE: 1995-60-0
EARLIER FILING DATE: 1995-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PRELICATION NUMBER: 07/550,837
EARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PRELICATION WINDER: 07/550,837
EARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PRELICATION WINDER: 07/550,837
ERIGHTH: 50
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Job time : 29.8667 secs
RESULT 15
US-09-168-947-9
Sequence 9, Application US/09168947
Patent No. 6589734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 13516, A Sequence 13516, A Sequence 15330, A Sequence 15330, A Sequence 27147, A Sequence 27147, A Appl Sequence 1140, Appl Sequence 1340, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 626, Appl Sequence 626, A

Sequence 31632, A Sequence 31632, A Sequence 1097, Ap Sequence 1097, Ap Sequence 1099, Ap Sequence 1098, Ap Sequence 1098, Ap Sequence 33668, A Sequence 41653, A Sequence 416

Scoring table:

Searched:

Database

Title: Perfect score:

Sequence:

OM nucleic

Run on:

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APPLICANT: Duke University
APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Bruce
APPLICANT: Sullenger, Christopher
TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
FILE REFERENCE: 180/124/2
CURRENT APPLICATION NUMBER: US/09/963,827B
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,654
PRIOR APPLICATION NUMBER: 60/235,654
NUMBER OF SEQ ID NOS: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 34;
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             5 US-10-027-632-178287
5 US-10-027-632-178287
6 US-00-027-632-178299
6 US-00-085-783A-15330
1 US-09-842-751-747
7 US-09-842-751-747
8 US-09-842-751-747
8 US-09-842-751-747
8 US-09-842-751-75
8 US-09-842-751-75
8 US-09-815-242-75
8 US-09-915-28
9 US-09-91-56-808-16
9 US-09-91-58-808-16
9 US-09-91-58-808-16
9 US-09-91-91-91
10 US-09-818-875-1098
11 US-10-209-787-1098
12 US-10-209-787-1098
13 US-10-21-185-1097
14 US-10-21-185-1098
15 US-10-21-185-1098
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US-10-424-599-41653
US-10-424-599-133545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70, Application US/09963827B Publication No. US20030175703A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(34)
COTHER INFORMATION: RNA aptamer
US-09-963-8278-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: RNA aptamer
                                                                                                                                                                                                                      01066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
 RESULT 1
US-09-963-827B-70
                   LENGTH: 34
 RESULT
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Sequence 2, Appli
Sequence 39, Appli
Sequence 317, App
Sequence 317, App
Sequence 317, App
Sequence 317, App
                                                                                                                       April 9, 2004, 03:53:35 ; Search time 420.8 Seconds (without alignments) 303.112 Million cell updates/sec
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Sequence 41,
Sequence 26,
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Sequence 19,
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'(gn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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'(gn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-155-233-1

US-10-155-233-19

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US-09-963-827B-3

US-09-963-827B-3

US-09-963-827B-3

US-09-850-716A-317

US-09-850-778-317

US-09-850-778-317

US-09-850-778-317

US-10-117-982-317

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US-10-117-982-317

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US-10-155-233-26

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                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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Maximum DB seq length: 200
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Gaps

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US-09-963-827B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Aptamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Aptamer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence and supplication US/10155233
sublication No. US20030083294A1
sublication No. US20030083294A1
sublication No. US20030083294A1
sublication No. US20030083294A1
sublication Sullanger, BRUCE A
subplicant: Sullanger, BRUCE A
subplicant: RUSCONI, CHRISTOPHER
TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
FILE REFERENCE: 1579-684
current Application NUMBER: US/10/155,233
current Application NUMBER: 60/293,231
prior Filing DATE: 2001-05-25
prior RILING DATE: 2001-0-25
prior RUSCATION NUMBER: 60/331,037
prior RUSCATION NUMBER: 60/331,037
prior RUSCATION NUMBER: 60/331,037
prior RUSCATION NUMBER: 2001-11-07
submber OF SEQ ID NOS: 41
subplication Ver. 2.1
subplication Ver. 2.1
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US-10-155-233-1
; Sequence 1, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
APPLICANT: SULENGER, BRUCE A
; TITLE OF INVENTION: CHRISTOPHER
; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
; FILE REFERENCE: 1579-684
; CURRENT APPLICATION NUMBER: US/10/155,233
; CURRENT APPLICATION NUMBER: 60/293,231
PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PATENTIN VOR: 2.1
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100.0%; Score 34; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 34; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.2e-06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 34; Conservative
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| LOCATION: (35)
| OTHER INFORMATION: N=idT
US-10-155-233-1
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LENGTH: 35
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Sequence 3, Application US/09963827B

Publication No. US20030175703A1

GENERAL INFORMATION

APPLICANT: Duke University

APPLICANT: Rusconi, Christopher

TITLE OF INVENTION: RA APTAMERS AND METHODS FOR IDENTIFYING THE SAME

TITLE OF INVENTION NUMBER: US/09/963,827B

CURRENT FILING DATE: 2001-09-26

FRICH FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 227

SOFTWARE: Patentin version 3.0

SEQ ID NO 3

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 34; DB 14; Length 40; Best Local Similarity 100.0%; Pred. No. 7.3e-06; Matches 34; Conservative 0; Mismatches 0; Indels
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          PUDLICATION NO. USCOURS.

PUDLICATION NO. USCOURS.

GENERAL INFORMATION:

APPLICANT: SULENGER, BRUCE

APPLICANT: RUSCONI, CHRISTOPHER

TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS

FILE REFERENCE: 1579-684

CURRENT PILING DATE: 2002-05-28

PRIOR PLLING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/293,231

PRIOR APPLICATION NUMBER: 60/331,037

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 2

LENGTH: 40
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Sequence 2, Application US/10155233 Publication No. US20030083294A1
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LOCATION: (1)...(96)
CTHER INFORMATION: RNA aptamer
US-09-963-827B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: RNA aptamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Artificial Sequence
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104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133
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CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 317, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Mang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 56.7
Matches 17; Conservative
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Matches 17; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapien
    US-09-850-716A-317
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US-09-897-778-317
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US-10-117-982-317
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-10-155-233-29
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Mosil, Particia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45514
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT APPLICATION NUMBER: US/09/735,705
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
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           Sequence 29, Application US/10155233

Publication No. US20030083294A1

GENERAL INFORMATION:
APPLICANT: SULLENGER, BRUCE A
APPLICANT: SULCENTS.
TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
FILE REFERENCE: 1579-664
CURRENT APPLICATION NUMBER: US/10/155,233
CURRENT PILING DATE: 2002-05-28
PRIOR PLLING DATE: 2001-05-25
PRIOR PLLING DATE: 2001-05-25
PRIOR PLLING DATE: 2001-10-7
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 23
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Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Fanger, Gary R.
Li, Samuel X.
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-10-155-233-29/c
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LENGTH: 196
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APPLICANT:
APPLICANT:
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Sequence 317, Application US/09850716A
Patent No. US20020115139A1
Patent No. US20020115139A1
Patent No. US20020115139A1
PAPLICANT: Machael D.
PAPLICANT: Machael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT APPLICATION NUMBER: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%; Score 17.2; DB 9; Length 196; 56.7%; Pred. No. 4.6e+02;
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APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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US-10-155-233-26/c
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LENGTH: 17
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                                                                                          APPLICANT: Fan, Gregory A.

APPLICANT: Fan, Ligun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C18

CURRENT APPLICATION NUMBER: US/10/117,982

CURRENT FILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 484

SOCTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 317

LENGTH: 196
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| Publication No. US20030236209A1
| GENERAL INFORMATION:
| APPLICANT: WCASTON AND APPLICANT: MCNAbb, Andria
| APPLICANT: MCNAbb, Andria
| APPLICANT: MCHARDA, Andria
| APPLICANT: MCHARDA, Andria
| APPLICANT: WCASTON AND MCTHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND MCTHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPRENCE: 210121.455C19
| CURRENT APPLICATION NUMBER: US/10/313,986
| CURRENT FILING DATE: 2002-12-04
| NUMBER OF SEQ ID NOS: 560
| SOFTWARE: FESTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 196;
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Publication No. US20030083294A1
GENERAL INFORMATION:
APPLICANT: SULLENCER, BRUCE A
APPLICANT: RUSCONI, CHRISTOPHER
TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
FILE REFERENCE: 1579-684
CURRENT APPLICATION NUMBER: US/10/155,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.6%; Score 17.2; DB 14; Best Local Similarity 56.7%; Pred. No. 4.6e+02; Matches 17; Conservative 5; Mismatches 8;
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                                  Watanabe, Yoshihiro
Henderson, Robert A.
Kalos, Michael D.
Mericle, Barbara
Spies, Gregory A.
Vedvick, Thomas S.
                     Darrick
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Best Local Similarity 56.7
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-10-117-982-317
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CORGANISM: Homo sapiens
US-10-313-986-317
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US-10-155-233-25/c
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LENGTH: 196
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; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-25
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US-10-155-233-41
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i Sequence 41, Application US/10155233

j Publication No. US20030083294A1

i GENERAL INFORMATION:

APPLICANT: SULLENGER, BRUCE A

TITLE OF INVENTION: CHRISTOPHER

TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS

FILE REFERENCE: 1579-684

CURRENT APPLICATION NUMBER: US/10/155,233

CURRENT FILING DATE: 2002-05-28

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTING DATE: 2001-11-07
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Publication No. US20030083294A1

GENERAL INFORMATION.

APPLICANT: SULLENGER, BRUCE A

APPLICANT: RUSCONI, CHRISTOPHER

TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS

FILE REFERENCE: 1579-684

CURRENT APPLICATION WUMBER: US/10/155,233

CURRENT FILING DATE: 2001-05-28

PRIOR APPLICATION NUMBER: 60/293,231

PRIOR PILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25
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50.0%; Score 17; DB 14; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.38+02;
Matches 14; Conservative 3; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 14; Length 17;
Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293,231
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/331,037
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 17
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17 TAATGCTGCCTCCCCAT 1
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17 ATGGGACTATACCGCG 1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 70.69
Matches 12; Conservative
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                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-10-155-233-26
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; Publication No. US20030083294A1
; GENERAL INFORMATION:
; APPLICANT: SULLENGER, BRUCE A
; APPLICANT: SULLENGER, BRUCE A
; APPLICANT: RUSCOVI, CHRISTOPHER
; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
; FILE REFRENCE: 1579-684
; CURRENT APPLICATION NUMBER: US/10/155,233
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,231
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
LENTH: 20
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ORGANISM: Artificial Sequence
FEATURE:
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 18
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US-10-155-233-20/c
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Search completed: April 9, 2004, 10:11:30 Job time: 420.8.8ecs

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18.6 54.7 145 9 AIB73178 18.6 54.7 175 12 BI781660 18 52.9 92 13 BU648134 18 52.9 175 9 AA249214	17.8 52.4 194 9 AV011213 17.6 51.8 119 28 AZ25888 17.6 51.8 127 28 AZ121703 17.6 51.8 168 10 BB170705 17.4 51.2 97 29 CGG13410 17.4 51.2 160 14 CK296959	17.2 50.6 56 28 AZ512563 17.2 50.6 80 13 BQ918470 17.2 50.6 107 13 BQ924632 17.2 50.6 111 13 BQ824632 17.2 50.6 143 12 B1998642 17.2 50.6 149 9 AV390541	17.2 50.6 155 13 BQ808240 17.2 50.6 160 13 BQ824080 17.2 50.6 161 13 BQ82227 17.2 50.6 162 12 B1996058 17.2 50.6 162 13 BQ824649 17.2 50.6 163 10 AM146518	17.2 50.6 172 12 BI997268 17.2 50.6 175 13 BQ811695 17.2 50.6 177 13 BQ824879 17.2 50.6 177 12 B1720254	33 17.2 50.6 185 12 B1816617 B1816617 1031063A1 34 17.2 50.6 187 28 A2372216 MO124A05 35 17.2 50.6 196 13 B0825311 B0825311 B0825311 B0825311 B0825311 B030125H0 37 17.2 50.6 196 13 B0825311 B0825311 B0825311 B0825311 B030125H0 3 17.2 50.6 196 13 B082685 CF296285 300G8H1 4 17 50.0 165 28 AQ304066 BR934674 BF014058 BR934674 BF014058 BR946477 BF994058 BC1-UT008 42 16.8 49.4 181 12 BR946477 BF994058 BR946477 BF995024 BF994058 BF994058 BF994058 BF994058 BF994058 BF9940511.8 BF994058 BF994058 BF9940511.8 BF994058 BF9940511.8 BF9950024 BF9950024 BF9950024	ALIGNMENTS	CG733695 CG733695 108 bp	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. REFERENCE 1 (bases 1 to 108) AUTHORS Walbot, V. TITLE Maize genomic sequences found using engineered RescueMu transposon	Unpublished (2001) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227	Fax: 550 725 8221 Email: walbordestanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1119158 row: 8
							RESUL- CG733 LOCUS DEFIN ACCESS VERSIC SOURCE SOURCE	REFERI AUTH	COMMEI	····
5.1.6 Compugen Ltd.	Search time 1040.4 Seconds (without alignments) 975.888 Million cell updates/sec	cau 34	ев 3354136					d by chance to have a the result being printed,	istribution. Description	CG733695 1119158F0 CG733696 1119158F0 BE183096 CM2-HT065 AW997328 RC2-BN004
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compu	search, using sw model 1 9, 2004, 02:50:24 ;	US-09-963-827B-70 34 1 augggacuauaccgcguaaugcugccucccau IDENTITY_NUC Gapop 10.0 , Gapext 1.0	27513289 seqs, 14931090276 residue f hits satisfying chosen parameters: length: 0 length: 200	Minim Maxim Listir		14: go est3:* 13: gb_est4:* 14: gb_est5:* 15: em_estfun:*	16: em_edcom:* 17: em_gas_hum:* 18: em_gas_hum:* 19: em_gas_pln:* 21: em_gas_fun:* 22: em_gas_fun:* 23: em_gas_fun:* 23: em_gas_fun:* 24: em_gas_fun:* 25: em_gas_fun:* 26: em_gas_fun:* 26: em_gas_fun:* 27: em_gas_fun:* 28: em_gas_fun:* 28: em_gas_fun:*	the god	l by analysis y y Length DB	57.1 108 29 CG733695 57.1 108 29 CG733696 55.3 179 10 BE183096 55.3 188 10 AW997328
	OM nucleic - nucleic Run on: Apri	Title: Perfect score: 3 Sequence: 1 Scoring table: I	Searched: 2 Total number of h Minimum DB seq le	ocessing:	Database:	7885			and is deri Result O No. Score M	1 19.4 2 19.4 3 18.8 6 4 18.8

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BE183096.1 GI:8662272
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                                                                                                                                                                                                                                                                                                                      19; Conservative
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COMMENT
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BE183096
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                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                          /tissue_type="leaf"
/dev stage="adult"
/lab_host="blutus"
/done lib="1119 - RescueMu Grid AA"
/done lib="1119 - RescueMu Grid AA"
/done lib="1119 - RescueMu Grid AA"
/done="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site l: BamHi; Site 2: BglII;
RescueMu is a 4.9 bb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHi and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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/mol type="genomic DNA"
/mol type="genomic DNA"
/molltivar="mixed background W23/A188/B73/K55"
/tissue[='taxon:4577"
/tissue[type="leaf"
/dev stage="adult"
/lab-host=="DH10B"
/clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
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                                                                          mol type="genomic DNA"
culLivar="mixed background W23/A188/B73/K55"
db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plates with ampicillin."
                                                          'organism="Zea mays"
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Location/Qualifiers
                    Location/Qualifiers
Class: transposon-tagged
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Matches 19; Conserv
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DEFINITION
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JOURNAL
COMMENT
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KEYWORDS
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pBlueScript backbone); Site 1: BamH1; Site 2: BglII; RescueWu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Wu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zamb.iastete.edu' and follow the links for RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamH1 and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM2-HT0655-170 Seq primer: puc 18 forward 400-157-h05&t3=2000-04-178t4=1)

High quality sequence start: 36

High quality sequence start: 36

High quality sequence story: 178.
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//mol type="mmna" orgina.../
/dov stage="Adult" |
/dov stage="Adult" |
/dov stage="Adult" |
/dov plane lib="HT0655" |
/note="Organ: head neck; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 179)
1 (Bases 1 to 179)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Go'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HE183096 170400-157-h05 HT0655 Homo sapiens CDNA, mRNA sequence.
BE183096
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S7.1%; Score 19.4; DB 29;
Similarity 65.5%; Pred. No. 9.7e+02;
19; Conservative 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 GGACUAUACCGCGUAAUGCUGCCUCCCCA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B GAACTCTACCGCGCCATGCTGCCGCCTCA 36
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/organism="Homo sapiens"
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ORIGIN

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Contact: Robert Strausberg, Ph.D.

Email: cgapba-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 760 Std Error: 0.00
Seq primer: -40UP from Gibco

High quality sequence stop: 142.
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                                                                                                                                145 bp mRNA linear EST 17-DEC-1999 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321787 3',
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                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 145)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Ascaris suum
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AUGGGGACUAUACCGCGUAAUGCUGCCUCCCCA 33
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2321787"
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                                                                                                                                                                                                                                                                     AI873178.1 GI:5547227
                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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Unpublished (1997)
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                                                                                                                                                                                                         mRNA sequence.
AI873178
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                                                                                                                                       AI873178
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KEYWORDS
SOURCE
ORGANISM
                                                                     RESULT 5
AI873178/c
                                                                                                                                                                   DEFINITION
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BI781660/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fins sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL: (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=RC2-BN0048-250 400-019-h08&£13-2000-04-25£t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 188.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="manny" apprens
/mol_type="manny" apprens
/db_xref="taxon:9606"
/de_stage="Adult"
/clone_lib="BN0048"
/note="Organ: breast normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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1 (bases I to 188)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Erunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Singson,A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW997328 15-JUN-2000 188 bp mRNA linear EST 05-JUN-2000 RC2-BN0048-250400-019-h08 BN0048 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                    Length 179;
                                                                                                                                                                   Indels
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                                                                                              Score 18.8; DB 10;
Pred. No. 2e+03;
6; Mismatches 7;
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Pred. No. 2e+03;
4; Mismatches 7;
low stringency conditions."
                                                                                                                                                                                                                              2 UGGGGACUAUACCGCGUAAUGCUGCCUCCC 31
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/organism="Homo sapiens"
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                                                                                              Query Match
Best Local Similarity 56.7%;
Matches 17; Conservative
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Homo sapiens
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Matches 19; Conserv
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JOURNAL MEDLINE PUBMED

COMMENT

TITLE

FEATURES

ORIGIN

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ACCESSION

RESULT 4

ò 셤 VERSION KEYWORDS

REFERENCE AUTHORS ö

Gaps

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Harvard Medical School 75 Francis St. Boston, MA 02115, USA Tel: 6177328915
                                                                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                            Duke University
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Best Local Similarity
Matches 18; Conserv
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AA249214
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                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800

Fax: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu

The library was constructed by Brandi Chiapelli and Dr. James

The library was constructed by Brandi Chiapelli and Dr. James

McGarter at Washington University, St. Louis. The cDNA was made by

using Dynabead oligo-dr priming (Dynal). PCR based library using a

modified protocol from the SNART PCR cDNA Synthesis Kit from

Clontech. Directionally cloned into the UDG sites of pAMP1.

Dissected nematode tissues were provided by Dr. Alan Scott

(ascott@jhaph.edu). of the School of Public Hygene and Public Health

at John Hopkins University in Baltimore, MD.

Seg primer: -40RP from Gibco

High quality sequence stop: 156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pamp1 (Gibco); Site 1: Not1; Site 2: Sal1;
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
cDNA was made by using Dynabead oligo-dT priming (Dynal).
PCR based library using a modified protocol from the SNARY.
PCR cDNA Synthesis Kit from Clontech. Directionally cloned
into the UDG sites of pAMP1. Dissected nematode tissues
were provided by Dr. Alan Scott (ascott@jhsph.edu) of the
School of Public Hygene and Public Health at John Hopkins
University in Baltimore, MD."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Dissected female gonad (MZ=maturation zone, most proximal region of gonad)"
/dev_stage="Adult"
/lab_host="DH10B"
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                     1 (bases 1 to 175)

McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Wylie,T., Dante,M., Marra,M., Hiller,L., Ranklin,C.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
McCank,R., Rohn,S., Shin,T., Jackson,Y., Cardenas,M.,
The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                              Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'clone lib="Ascaris suum female gonad MZ pAMP1 v2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ascaris suum"
/mol type="mRNA"
/db_xref="taxon:6253"
/sex="Pemale"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chiapelli McCarter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU648134
BU648134.1 GI:23360314
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BU648134
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/mol_type="mcMnA"
/mol_type="mcMnA"
/mol_type=mth."
/db_xrain="21gr (CC-1690 wild type mt+) & 6145c (CC-1691
wild type mt-)"
/db_xref="taxon:305s"
/db_xref="taxon:305s"
/db_xref="taxon:305s"
/clone lib="decorated by the color type mt-),
Gamete="vector: pBluescript II SK-; Site_I: EcoRI; Site_2:
/note="vector: pBluescript II SK-; Site_I: EcoRI; Site_2:
Xhol; Gamete library was constructed by Hui Zhao, Min Lu,
Jeffrey McDermott, William J. Snell and John Davies.
Strain 21gr cells (CC-1690; mething type plus) and strain
6145c cells (CC-1690; mething type plus) and strain
Growing on a light-dark cycle (13:11 L/D) in R-medium
(Sager and Granick) were separately transfered into
nitrogen-free medium at 8 hours into the light period.
PolyA mRNA was purified from each sample every 2 hours for
the next 18 hours. The mRNA was pooled and used for CDNA
synthesis. The CDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5:) and XhoRI (3:)
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with ExABsiste
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
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hisoloon seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
AA249214
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175)
Chlamydomonadaceae; Chlamydomonas.

I (Dases 1 to 93.

Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 3.6e+03;
...-rahes 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Chlamydomonas reinhardtii"
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Unpublished (1997)
Contact: Liew CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: chauser@duke.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                   Contact: Charles Hauser
DCMB Box 91000
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Tel: 919 613 8159
Fax: 919 613 8177
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60.0%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E. (bases 1 to 119)
S. Zhao, S., Nierman; W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mogann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-11211.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ258888 linear GSS 26-JUL-2000 RPCI-23-11211.TV RPCI-23 Mus musculus genomic clone RPCI-23-11211,
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_l:
EcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Feierer de Jons

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 112 row: I column: I

Seq primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                Gaps
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                                                                          /dev_stage="18-day embryo"
/clone_lib="Mus musculus 18-day embryo C57BL/6J"
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                                                                                                                                                                                                             Length 194;
                                                                                                                                                                                                         52.4%; Score 17.8; DB 9; Length 1
58.6%; Pred. No. 5.4e+03;
ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                   5 GGACUAUACCGCGUAAUGCUGCCUCCCCA 33
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/organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="RPCI-23-11211"
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          /clone="1110030P07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
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GSS.
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                                             /sex="mixed"
                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                            Best Local Similarity
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AZ258888/c
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Fax: 81-298-36-9145
Fax: 81-298-36-909
Fax: 81-298-36-909
Email: genome-resertc riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehablose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 194)
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                                                     PURP PRIMERS
PORMARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seg primer: 5' GAAATTAACCCTCACTAAAGGG 3'
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.9%; Score 18; DB 9; I ilarity 50.0%; Pred. No. 4.3e+03; Conservative 7; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .175
/organism="Homo sapiens"
                                   cliew@rics.bwh.harvard.edu
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Fax: 6179750995
Email: cliew@ri
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DEFINITION

AZ121703

ð g ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Email: genome-rasegec.riken.go.jp,
URL:http://genome.gec.riken.go.jp,
URL:http://genome.gec.riken.go.jp/
URL:http://genome.gec.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoattivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Okawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system Genome Res. 9 (5), 463-470 (1999)
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                S Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
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Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, Y., Shibata, Y., Shigamoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
Takahashi, P., Tominaga, N., Toya, T., Tsunoda, Y., Wataniki, A.,
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Hayashizaki, Y., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
Hayashizaki, Y.
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fel: 81-45-503-9222
Fex: 81-45-503-9226
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bages 1 to 168)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for
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/dev_stage="adult"
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/clone_lib="RIKEN full-length enriched, adult male
hypothalamus"
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                                                                                                Mus musculus (house mouse)
                                    GI:8829788
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                                 BB170705.1
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                                                                                                                                  ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                    SOURCE
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Stao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1993)
Other 2858: RECI-23-479G20.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: stao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@reegen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primmer: 479 row: G column: 20
                                                                                                                                                                                                                               GSS 12-MAY-2000
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/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
1 (bases 1 to 127)
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RPCI-23-479G20.TV RPCI-23 Mus musculus genomic clone RPCI-23-479G20, genomic survey sequence.
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                                        63 TGGGGACTTTACAGCTCTCTGCTGCTTACTCA 32
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/clone="RPCI-23-479G20"
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/strain="C57BL/6J"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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FEATURES

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Matches

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SM Nicociana benthamiana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 160)
S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other. ESTS: ESTSS672
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 challenged leaves (Pseudomonas syringae pv tomato 12 hr; Azathomonas campestris pv campeetris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"

Lab host="DHIOB-TOAA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, hear-stressed leaves (8 C, 3 hr, 6hr), and pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 56)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Diderhausern, A. and Wright, D., Weise, R., Tingey, A., von Diserts Innih iserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ512563 16b DNA linear GSS 05-OCT-200 IM0358G13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0358G13 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   these tissues and pooled in approximately equal molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 51.2%; Score 17.4; DB 14; Length 160; I Similarity 59.3%; Pred. No. 7.5e+03; 16; Conservative 5; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 160
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMD548"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CUAUACCGCGUAAUGCUGCCUCCCCAU 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
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                                   Nicotiana benthamiana
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S. Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., van Sligenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Whal kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC\ I. "
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                                                                                                                                                                                                   Gaps
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OST300555 Mus musculus 129Sv/Ev Mus musculus genomic clone OST300555, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
                                                                                                                                            DB 10;
                                                                                                                                   Score 17.6; DB 10;
Pred. No. 6.3e+03;
7; Mismatches 9;
                                                                                                                                                                                                                                                                                  118 ATGCGGACTATGACCTGTGATACTACCTTCCC 149
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/mol type="genomic DNA"
/strain="129SV/EV"
/db_xref="taxon:10090"
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Location/Qualifiers
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CK296959
CK296959.1 GI:39882864
                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 16; Conservative
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SOURCE ORGANISM

VERSION KEYWORDS ACCESSION

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

ORIGIN

DEFINITION RESULT 13 CG613410

LOCUS DEFINITION

RESULT 14 CK296959

ACCESSION VERSION

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Gaps

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/db xref="taxon:1000"
/clone="UUGCIM0358G13"
/clone="UUGCIM0358G13"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources Adocuments/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|473214|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                        5
                                 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7000
Flate: 0358 row: G column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 56.
                                                                                                                                                                                                                                                                                                                                                                                                                               1. .56
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
University of Utah
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0; Gaps Query Match 50.6%; Score 17.2; DB 28; Length 56; Best Local Similarity 63.6%; Pred. No. 6.7e+03; Matches 14; Conservative 5; Mismatches 3; Indels ઠે

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Search completed: April 9, 2004, 06:03:59 Job time: 1044.9 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES DB ID Description		6 AR051528 AR051528 Sequence 6 AR072668 Sequence	AR073213	G43342	AX923424	AB059077	ECY17989	AX694803	AF178265S1	AF178269S1	AF178273S1	S6/413 DX68333	AR058826	AR063552	AR140942	AA86/991 BD148053	F320227816	F320227S10	ARUSIS4 / AR072687	AR073232	AR171238	HSMC24G11	AX164814	AF150996	6 BD261167 BD261167 Methods E	BD2/3668 BD139195	AB042992	AX902921	BD038454	DMI16691 HSII15687	HSU15686	AF064198	AF064199	AXZ483Z8 AR336716	AR176221	AX003193	ALIGNMENTS		iby bp DNA linear FAI 29-SEF-159 from patent US 5830670.	750 P		
\$ Query Score Match Length		19 65.5 169	9 65.5	7.8 61.4	.8 57.9	6.4 56.6	16 55.2	8 54.5 53.9	5.6	5.6 53.8	5.6 53.8	5.4 53.1 53.1	5.2 52.4	5.2 52.4	5.2 52.4	5.2 52.4	5.2 52.4	5 51.7	51.7	15 51.7	4.8 51.0	4.8 51.0	4.6 50.3	4.6 50.3	.6 50.3	4.6 50.3	4.6 50.3	4.6 50.3	4.6 50.3	4.6 50.3	4.6 50.3	4.6 50.3	4.6 50.3	4.4 49.7	4.4 49.7	4.4 49.7		/c	ARUSISZB 7 Sequence 98 ARUSISZB 75051528	ARUSIS28.1 GI:		M Unknown.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 101)

S Wang, D.G., Fan, J.B., Siao, C.J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, M., Winchester, E., Spencer, J., Kruglyak, L., Stein, L., Hsie, L., Topaloglou, T., Hubbell, E., Robinson, E., Mitchann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Lander, E.S.

Lange-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome

L. Science 280 (5366), 1077-1082 (1998)
                                                                           STS 27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR Cycles: 30
Thermal Cycler: custom built by IAS, Costar, Cambridge MA
                                                                         G43342 Innear STS 27-JAN-
WIAF-2007-STS Human THudson EST Homo sapiens STS cDNA, sequence
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/organism="Homo sapiens"
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/map="147.90 cR from top of Chr1 linkage group"
/clone_lib="Human THudson EST"
/note="STSs derived from sequences in dbEST and the Uniquene collection."
1. .101
1. .25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitehead Institute for Biomedical Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1900
Fax: 617 252 1900
Finer A: TAAAACATACGAGTACTGTACACGC
Primer A: TAAAACATACGAGTACTGTACACGC
Primer B: TCCCCTCCTGAATATACAACG
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Primer: each 5 pW
dNTPs: 4 nM
Tag Polymerase: 0.5 U
Total Vol: 20 uL
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50 mM
10 mM
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Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synonyms: CL_EST232115
Contact: Thomas Hudson
                                                                                                                                                         G43342.1 GI:4192259
                                                                                                                                                                                              Homo sapiens (human)
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Tris-HCl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gelatin:
                                                                                                                  tagged site.
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primer_bind
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PUBMED
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AUTHORS
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de la Monte, S. and Wands, J.R.
Neural thread protein gene expression and detection of Alzheimer's
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de la Monte, S. and Wands, J.R.
Neural thread protein gene expression and detection of alzheimer's
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                                                                                                                Query Match 65.5%; Score 19; DB 6; Length 169; Best Local Similarity 70.4%; Pred. No. 6.1e+02; Matches 19; Conservative 3; Mismatches 5; Indels
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Location/Qualifiers
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Location/Qualifiers

    169
/organism="unknown"
/mol_type="unassigned DNA"

                                                                                                                                                                                                                                                                                                                             Sequence 98 from patent US 5948634.
                1. .169
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Sequence 98 from patent US 5948888.
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/organism="unknown"
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AR073213.1 GI:9999976
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1. .20
/PCR conditions="denaturation 30s at 95 degrees, annealing 70s at 57 degrees, extension 30s at 72 degrees, final elongation 5min at 72 degrees, 35 cycles" complement(141. .160)
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Sus scrofa domestica genomic DNA, chromosome 10, 346B10F, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Paracanthopterygii, Gadiformes, Gaidropsaridae,
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                   Kiuchi,S., Inage,Y., Hiraiwa,H., Uenishi,H. and Yasue,H.
Assignment of 280 swine genomic inserts including 31
microsatellites from BAC clones to the swine RH map (IMpRH map)
Mamm. Genome 13 (2), 80-88 (2002)
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Direct Submission
Submitted (30-MAR-2001) Sachiko Kiuchi, National Institute
Submitted (30-MAR-2001) Sachiko Kiuchi, National Institute
Agrobiological Sciences, Genome Research Group; 2 Ikenodai,
Kukizaki machi, Inashiki-gun, Ibaraki 305-0901, Japan
(E-mail:sachikok@affrc.go.jp, Tel:81-298-38-8664,
Fax:81-298-38-8674)
Location/Qualifiers
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Sequence Characterization of a Unique Intergenic Spacer in Seaficormes Mitochondrial DNA
Mar. Biotechnol. 1 (5), 411-0415 (1999)
10522675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..160
/organiam="Sus scrofa domestica"
/mol type="genomic DNA"
/sub_species="domestica"
/db_xref="taxon:9825"
/chromssome="10"
                                                                                          Sus scrofa domestica (domestic pig)
Sus scrofa domestica
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/standard_name="346B10F"
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Sciurognathi, Muridae, Murinae, Mus.
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Sciurognathi, Muridae, Murinae, Mus
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Stem cell culture
Patent: WO 03080816-A 1 02-OCT-2003;
THE UNIVERSITY OF SHEFFIELD (GB)
Location/Qualifiers
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Patent: WO 03080816-A 2 02-OCT-2003;
THE UNIVERSITY OF SHEFFIELD (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="unassigned DNA"
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/db_xref="taxon:10090"
           1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
                                                                                                                                         Sequence 1 from Patent WO03080816.
AX923424
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Sequence 2 from Patent W003080816.
AX923425
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Direct Submission
Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
Location/Qualifiers
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Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
Location/Qualifiers
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                                                                                                                                                                                 Molecular epidemiology of genital Chlamydia trachomatis infection
in high-risk women in Senegal, West Africa
J. Clin. Microbiol. 38 (1), 138-145 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular epidemiology of genital Chlamydia trachomatis infection
in high-risk women in Senegal, West Africa
J. Clin. Microbiol. 38 (1), 138-145 (2000)
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Chlamydia trachomatis isolate CAS99 major outer membrane protein
(ompl) gene, variable domain 1.
                                                                         Chlamydia trachomatis
Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia.
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1 (bases 1 to 60)
                                                                                                                                Sturm-Ramirez, K., Brumblay, H., Diop, K., Gueye-Ndiaye, A., Sankale, J.L., Thior, I., N'Doye, I., Hsieh, C.C., Mboup, S. and
                                                                                                                                                                                                                                                                                                      Sturm-Ramirez, K., Brumblay, H., Diop, K., Gueye-Ndiaye, A., Sankale, J.L., Thior, I., N'Doye, I., Hsieh, C.C., Mboup, S. and
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Sturm-Ramirez, K., Brumblay, H., Diop, K., Gueye-Ndiaye, A.,
Sankale, J.L., Thior, I., N' Doye, I., Hsieh, C.C., Mboup, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="variable domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/isolate="CA46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      country="Senegal"
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 GI:6716617
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                                                       Chlamydia trachomatis
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 AF178261.1
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AF178265S1
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                               Direct Submission
Submitted (20-AUG-1998) S. Johansen, Institution University of
Tromso, Department of Molecular Cell Biology, IMB, University of
Tromso, 9037 Tromso, NORWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.7e+04;
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Patent: WO 03008583-A 430 30-JAN-2003;
Sagres Discovery (US)
Location/Qualifiers
                                                                                                                                1. .51
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/organelle="mitochondrion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 430 from Patent WO03008583. AX694803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                          14. .39
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                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                      'product="tRNA-Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="tRNA-Pro"
/product="tRNA-Pro"
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                                                                                                                                                                                                                                                                 <1. .13
/gene="tRNA-Thr"
                                                                                                                                                                                                                                                                                                                                                              10. .51
/gene="tRNA-Pro"
                                                                                                                                                                                                                                             gene="tRNA-Thr"
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(bases 1 to
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               Johansen, S.
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AF178261S1
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AX694803/c
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ACCESSION VERSION

REFERENCE AUTHORS

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FEATURES

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Gaps

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Direct Submission
Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
Location/Qualifiers
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                                                                                                                                                                                               Molecular epidemiology of genital Chlamydia trachomatis infection in high-risk women in Senegal, West Africa J. Clin. Microbiol. 38 (1), 138-145 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mphibia, Batzachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus
1. (bases 1 to 79)
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Translocation of repetitive RNA sequences with the germ plasm in
Xenopus oocytes
Science 262 (5140), 1712-1714 (1993)
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Chlamydia trachomatis
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
                                                                                                                                          Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A., Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
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Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
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    .60
    .coganism="Chlamydia trachomatis"
/mol type="genomic DNA"
/isolate="CA584"

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/mol_type="genomic RNA"
/db xref="taxon:8355"
/cell_type="oocyte"
1. .79
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|gene="omp1"
|note="variable domain 1"
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/country="Senegal"
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                    GI:6716629
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Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard
School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis isolate CAS43 major outer membrane protein AP178269
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Chlamydia trachomatis
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 60)
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2 C. Chases 1 to 60)
Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A.,
Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and
Kanki,P.J.
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/organism="Chlamydia trachomatis"
| Mool type="genomic DNA"
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/mol_type="genomic DNA"
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                                                                                       1. .60
/gene="omp1"
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/gene="omp1"
/note="variable domain 1"
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17 ATACAGGCAATAGTGCAGCTCC 38
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Homo sapiens
Eukarýota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          Primiano, T., Chang, B.D. and Roninson, I.B.
Reagents and methods for identifying gene targets for treating cancer

Cancer

THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)

Location/Qualifiers

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"
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Search completed: April 9, 2004, 03:53:30 Job time : 244.439 secs

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April 9, 2004, 01:39:24; Search time 103.035 Seconds (without alignments) 1195.685 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	1 29	100.0	29	9	ABN88558	Abn88558 Coaqulat	lati
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ALIGNMENTS

RESULT 1

RNA aptamer; identification; coagulation factor; angiopoietin; thrombin; ESF family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis; bypass graft surgery; se. Coagulation factor IXa (FIXa) aptamer SEQ ID NO:71. ABN88558 standard; RNA; 29 BP. 26-SEP-2001; 2001WO-US030004 26-SEP-2000; 2000US-0235654P G. (first entry) Sullenger BA, Rusconi WPI; 2002-479560/51. (UYDU-) UNIV DUKE. WO200226932-A2. 19-AUG-2002 Homo sapiens. 04-APR-2002. Synthetic. ABN88558; ABN88558

Novel RNA aptamers that selectively bind coagulation pathway factors, B2 family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.

E2F

Claim 14; Page 25; 216pp; English.

The present invention describes RNA aptamers (1,II,III) that selectively bind: (a) a cosqulation pathway factor; (b) an E2F family member; or (c) angiopoietin-1 (Angl) or Ang2, respectively, where (I), (II), (III) have a dissociation constent for the cosqulation pathway factor, an E2F family member, or Angl or Ang2 of about 20 nM or less (I), (II) and (III) have cardiant and cyrostatic activities. (I) are useful for modulating the biological activity of a cosqulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

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the biological activity of the coagulation pathway factor in the warm-blooded vertebrate is modulated. (I) are also useful for treating cardiovascular diseases in the mammal. (II) are useful for modulating E2F activity in a warm-blooded vertebrate. (II) are useful for modulating E2F anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting cell proliferation in a number of conficions e.g., intimal hyperplasia following bypass graff surgery. (III) are useful for modulating anglogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic research and therapeutic context. The aptamers are useful as diagnostic compactically bind, and for identifying substances to which they becifically bind, for isolating and purifying substances to which they bind, and as a separation reagent for retrieving the targets to which they becifically bind. Anna8488 to ABN88713 and ABBB1231 represent eventual expenses.
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inflammatory proliferative disease; hypoglycaemia; human;
coagulation Factor IXa; FIXa; ss.
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                                                   The present invention relates to a method for altering the affinity of a nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient or in vitro, or reversing the binding of the labelled ligand to a target tissue. The method comprises administering a modulator that binds to the the modulator under conditions such that the modulator that binds to the the modulator under conditions such that the modulator binds to the ligand, and thus alters the affinity of the ligand for the target molecule. The method is useful for treating a number of disorders e.g. infection, autoimmunity, tumours, inflammatory proliferative diseases and hypoglycaemia. The present sequence is an aptamer to human coagulation pactor IXa (FIXa aptamer), which was used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
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inflammatory proliferative disease; hypoglycaemia; ss.
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                                              The present invention relates to a method for altering the affinity of a nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient or in vitro, or reversing the binding of the labelled ligand to a target tissue. The method comprises administering a modulator that binds to the ligand to a patient receiving the ligand, or contacting the ligand with the modulator under conditions such that the medulator binds to the ligand, and thus alters the affinity of the ligand for the target molecule. The method is useful for treating a number of disorders e.g. infection, autoimmunity, tumours, inflammatory proliferative diseases and hypoglycaemia. The present sequence is an aptamer which was used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an B2F family member; or (c) angiopoletin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-blooded vertebrate (i) are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA aptamerį identification; coagulation factor; angiopoietin; thrombin; E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant; cell proliferation; intimal hyperplasia; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 29; DB 7; Length 33; 100.0%; Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33 BP; 8 A; 10 C; 8 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGGACUAVACCGGCAAUCGUGCAUCCCC 31
Example 3; Fig 10A; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Fig 1B; 216pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN88504 standard; RNA; 96 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2001; 2001WO-US030004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2000; 2000US-0235654P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation, intimbypass graft surgery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rusconi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-479560/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200226932-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN88504:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
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cardiovascular diseases in the mammal. (II) are useful for modulating E2F activity in a warm-blooded vertebrate. (III) are useful for modulating Anglor Anglor Anglor in a warm-blooded vertebrate. (I) are potent anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for inhibiting call proliferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for inhibiting angiogenesis. The RNA aptamers are also useful for diagnostic, research and therapeutic context. The aptamers are useful for diagnostic research and therapeutic context. The aptamers are useful so diagnostic creagents to detect the presence or absence of target substances to which they specifically bind, and for isolating and purifying substances to which they bind, and as a separation reagent for retrieving the targets to which they bind, and as a separation reagent for retrieving the targets to which they specifically bind. ABN88488 to ABN88131 and ABBB1231 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method for detecting the presence of neural thread protein (NTP) having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject comprises (a) contacting a sample from a human subject that is suspected of contacting the NTP with at least one molecule capable of binding to the protein; and (b) detecting any of the molecule bound to the protein. The binding molecule is selected from an antibody free of natural impurities, a monoclonal antibody or a binding fragment of either of these. The method may be used for diagnosing the presence of Alzheimer's disease, neuroectodermal tumours and a malignant astrocytoma in a human. A number of clones of neural thread protein were isolated from healthy 17-18 week old foetal human brain (HB) 2 year old temporal lobe neocortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of neural thread protein in diagnosis of Alzheimer's disease - also NTP DNA and protein sequences used in gene and anti:sense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 29; DB 6; Length 96; 100.0%; Pred. No. 0.00037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human neural thread protein genomic clone (G5dPst-M13R).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 96 BP; 28 A; 25 C; 28 G; 0 T; 15 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; Pred. No. 0.0
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 GGGGACUAVACCGGCAAUCGUGCAUCCCC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 22E; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT27772 standard; cDNA; 169 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De La Monte S, Wands JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding fragment; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-259865/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT27772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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The present invention describes RNA aptamers (1,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) andyobotein-1 (Angl) or Ang2, respectively, where (1), (II), (III) have a candiopotein-1 (Angl) or Ang2, respectively, where (I), (II) and (III) have a candiant and cytostatic activities. (I) are useful for modulating the cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the biological activity of the coagulation pathway factor in the warm-coagulation activity of the coagulation pathway factor in the warm-coagulation activity of the coagulation pathway factor in the warm-coagulation activity in a warm-blooded vertebrate. (III) are useful for modulating E2F activity in a warm-blooded vertebrate. (III) are useful for modulating anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. (II) are useful for intimal hyperplasia following bypass graft surgery. (III) are useful for modulating angiogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic reasarch and therapeutic context. The aptamers are useful as diagnostic reasarch and therapeutic context. The aptamers are useful so which they specifically bind, and for identifying substances to which they specifically bind, for isolating and purifying substances to which they
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aptamer; identification; coagulation factor; angiopoietin; thrombin; family; cardiant; cytostatic; cardiovascular disease; anticoagulant; l proliferation; intimal hyperplasia; angiogenesis;
and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:7.
                                                                                                                                 ö
                                                                                   Score 19; DB 2; Length 169;
Pred. No. 29;
                                                                                                                              5; Indels
                                           Sequence 169 BP; 48 A; 24 C; 41 G; 56 T; 0 U; 0 Other;
                                                                                                                            3; Mismatches
                                                                                                                                                                                                36 GGACCAAAGCGGCCATCGTGCCTCCCC 10
                                                                                                                                                                       3 GGACUAUACCGGCAAUCGUGCAUCCCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Fig 1A; 216pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2001; 2001WO-US030004.
                                                                                 Query Match
Best Local Similarity 70.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2000; 2000US-0235654P
                                                                                                                                                                                                                                                                                                                           ABN88494 standard; RNA; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sullenger BA, Rusconi CP;
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bypass graft surgery; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                      ABN88494;
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The polymorphic markers which have been isolated using the primers polymorphic markers which have been isolated using the primers represented in AAX09121-X10268 The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary sphenocytosis, von Willebrand's disease, tuberous sclerosis, hereditary cancemorrhagic telangiscteral, familial colonic polyposis, Bilers-Danios syndrome, osteogenesis imperfects, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous cystem, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid engages of the nervous continuance of segments can also be used to produce medicaments for the treatment or
                                                                                                                                                             ö
bind, and as a separation reagent for retrieving the targets to which they specifically bind. ABN88488 to ABN88713 and ABB81231 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX10269-X12937 are human DNA fragments which contain biallelic
                                                                                                                                                               .;
0
                                                                                                                       DB 6; Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 101 BP; 27 A; 23 C; 26 G; 24 T; 0 U; 1 Other;
                                                                               Sequence 96 BP; 24 A; 26 C; 30 G; 0 T; 16 U; 0 Other;
                                                                                                                             ;
1e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human biallelic polymorphic DNA fragment WI-18680.
                                                                                                            (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 195; 310pp; English.
                                                                                                                                                                                                    5 ACUAUACCGGCAAUCGUGCAU 25
                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                30 ACUAUACCGGUCAUCGUGCAU
                                                                                                                                                                                                                                                                                                                                               AAX11804 standard; DNA; 101 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang D, Hudson T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US020313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylaxis of such diseases
                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-1999 (first entry)
                                                                                                                                                               19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment; marker; ss
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                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                      AAX11804;
                                                                                                                       Query Match
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                       RESULT 7
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1 GGGGACUAUACCGGCAAUCGUGCAUCCC 28

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The present sequence is that of the mouse indicolates growin Lactors, true present sequence is that of the mouse indication factor binding motifs ADE35058-ADE35060 from FGF-4 promoters have been shown to direct stem cell specific expression. This discovery was exploited in methods of the invention for manipulating the phenotype of a stem cell. In such a method, a cell is transfected with a mucleic acid molecule that includes the promoter which comprises a motif that confers stem cell specific expression on a selectable marker (e.g. fluorescent protein or produce cativating polypeptide) gene, and conditions conducive to proliferation of the cell are provided. A cell culture system is provided which facilitates the maintenance of stem cells, particularly embryonic stem cells, in an undifferentiated state. Also provided are differentiated cells and tissues, the genome of which includes a nucleic acid construct comprising a promoter which has a stem cell specific expression pattern which has a stem cell specific expression pattern comprising a promoter which have de-differentiated to a stem cell conferned cells. The stem cells are hammatopoletic, neural, bone, muscle, mesenchymal, trophoblastic, epithalial, endodermal or embryonic confermation of cells (including embryonal carcinoma TERA2 or NTERA2 cells), or manipulation of cells (including embryonal carcinoma TERA2 or NTERA2 cells), or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of the mouse fibroblast growth factor-3 (FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manipulating phenotype of stem cell by providing cell transfected with nucleic acid comprising promoter which confers substantial stem cell specific expression on selective marker gene(s), and proliferating cell.
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Fibroblast growth factor-4; FGF-4; mouse; stem cell; promoter; ds.
                                                    ö
            ); DB 2; Length 101;
1e+02;
                                                7; Indels
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            Score 17.8; DE Pred. No. 1e+024; Mismatches
                                                                                                                                                                                                                                                                                                                                             Mouse fibroblast growth factor-4 promoter.
                                                                                     Disclosure, Fig 2; 40pp; English.
                                                                                                                                                                                                                           ADE35061 standard; DNA; 166 BP.
            61.4%;
62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-2003; 2003WO-GB001111.
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08-MAY-2002; 2002GB-00010458
                                                                                                                                                                                                                                                                                                      (first entry)
Ouery Match
Best Local Similarity 62.19
Warrhes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Draper J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embryonal germ cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-779256/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003080816-A2.
                                                                                                                                                                                                                                                                                                        29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2003
                                                                                                                                                                                                                                                                 ADE35061;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                        RESULT
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The present sequence is that of the mouse fibroblast growth factor-3 (FGF -4) promoter from nucleotides -64 to +116. Transcription factor binding motifs ADE35058ADE35060 from FGF-4 promoters have been shown to direct stem cell specific expression. This discovery was exploited in methods of the invention for manipulating the phenotype of a stem cell. In such a method, a cell is transfected with a nucleic acid molecule that includes a promoter which comprises a motif that confers stem cell specific expression on a selectable marker (e.g. fluorescent protein or prodrug control propeptide) gene, and conditions conductve to profiferation of the cell are provided. A cell culture system is provided which cells; in an undifferentiated state. Also provided are differentiated confiring the genome of which includes a nucleic acid construct comprising a promoter which has a stem cell specific expression pattern which has a stem cell specific expression pattern which has estem cell specific expression pattern which have de-differentiated to a stem cell chance, thereby allowing their removal from a population of a memory of a differentiated cells. The stem cells are haemstoppietic, neural, bone, contain a contain contains the contains contains the contains 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manipulating phenotype of stem cell by providing cell transfected with nucleic acid comprising promoter which confers substantial stem cell specific expression on selective marker gene(s), and proliferating cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle, mesenchymal, trophoblastic, epithelial, endodermal or embryonic stem cells (including embryonal carcinoma TERA2 or NTERA2 cells), or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                   Fibroblast growth factor-4; FGF-4; mouse; stem cell; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.9%; Score 16.8; DB 9; Length 181; 60.7%; Pred. No. 3.4e+02; ive 4; Mismatches 7; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 181 BP; 27 A; 63 C; 62 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Db ..
3.4e+02;
                                                                                                                                                                                                                                                                                                            Mouse fibroblast growth factor-4 promoter.
1 GGGGACUAUACCGGCAAUCGUGCAUCCC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GGGGACTATCCCGCCACCGTTGCGTCCC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-2002; 2002GB-00006422.
08-MAY-2002; 2002GB-00010458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2003; 2003WO-GB001111
                                                                                                                                                    ADE35062 standard; DNA; 181
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 60.7
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYSH-) UNIV SHEFFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews P, Draper J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           germ cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-779256/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003080816-A2
                                                                                                                                                                                                                                                          29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2003.
                                                                                                                                                                                                         ADE35062;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                   RESULT 9
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Gaps

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57.9%; Score 16.8; DB 9; Length 166; 60.7%; Pred. No. 3.4e+02; ive 4; Mismatches 7; Indels (

Query Match 57.9 Best Local Similarity 60.7 Matches 17; Conservative

aptamer; identification; coagulation factor; angiopoietin; thrombin; family; cardiant; cytostatic; cardiovascular disease; anticoagulant; proliferation; intimal hyperplasia; angiogenesis;

cell proliferation; intim bypass graft surgery; ss.

RNA EZF

Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:12.

(first entry)

19-AUG-2002

ABN88499;

ABN88499 standard; RNA; 95 BP.

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The present invention relates to a method for altering the affinity of a nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient or in vitro, or reversing the binding of the labelled ligand to a target tissue. The method comprises administering a modulator that binds to the ligand to a patient receiving the ligand, or contacting the ligand with the modulator under conditions such that the modulator binds to the ligand, and thus alters the affinity of the ligand for the target molecule. The method is useful for treating a number of disorders e.g. infection, autoimmunity, tumours, inflammatory proliferative diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypoglycaemia. The present sequence is an aptamer to human coagulation Factor IXa (FIXa aptamer), which was used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altering affinity of nucleic acid ligands for target molecules in a patient or reversing binding of labeled ligands to target tissues, by administering (to a patient receiving the ligand) a modulator that binds
                                                                                                                                               Immunosuppressive; aptamer; infection; autoimmunity; tumour; inflammatory proliferative disease; hypoglycaemia; human; coagulation Factor IXa; FIXa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.2; DB 7; Length 29;
Pred. No. 5.1e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                      .29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29 BP; 8 A; 8 C; 8 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                         1. .5
/*tag= a
/bound moiety= "Nucleotides 25.
11. .21
^*tag= b
                                                                                                                                                                                                                                                                                                                             25. .29
/*tag= c
/bound_moiety= "Nucleotides 1.
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 7; 111pp; English
                             멾.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001; 2001US-0293231P. 07-NOV-2001; 2001US-0331037P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-2002; 2002WO-US016555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 55.9%;
l Similarity 72.4%;
21; Conservative (
                            ABZ21255 standard; RNA; 29
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sullenger BA, Rusconi C;
                                                                                                                    FIXa aptamer, SEQ ID 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-140438/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                          WO200296926-A1
                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                       misc_binding
                                                                                                                                                                                                                                                                                                                                misc_binding
                                                                                       16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-2002
                                                                                                                                                                                                                                                                                                 stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                         ABZ21255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
RESULT 10
               ABZ2125
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Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Angl or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Angl or Ang2 activity in a mammal.

GĐ;

Rusconi

Sullenger BA,

(UYDU-) UNIV DUKE.

WPI; 2002-479560/51.

26-SEP-2001; 2001WO-US030004 26-SEP-2000; 2000US-0235654P

WO200226932-A2

04-APR-2002

Homo sapiens Synthetic.

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The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiopoletin-I (Angi) or Angi, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Angi or Angi of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that the blooded vertebrate is modulated. (I) are useful for reading cardiovascular diseases in the mammal. (II) are useful for reading cardiovascular diseases in the mammal. (II) are useful for modulating and significantly delay the clotting time of normal human cartivity in a warm-blooded vertebrate. (II) are potent anticoagulants and significantly delay the clotting time of normal human cartivity in a varm-blooded vertebrate. (II) are spotent context on the activation of platelets in response to thrombin. (II) are useful for inhibiting cell proliferation in a number of conditions e.g., intimal hyperplasia following bypass graft surgery. (III) are useful for modulating angiogenesis. The RNA aptamers are also useful for diagnostic research and therapeutic context. The aptamers are useful as diagnostic reagents to detect the presence or absence of target substances to which they specifically bind, and for identifying substances to which they specifically bind, ABN8488 to ABN89713 and ABBS121 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.2; DB 6; Length 95;
Pred. No. 6.1e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95 BP; 25 A; 26 C; 29 G; 0 T; 15 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 GGGGACUAUACGUGAACGACUGCAUCCAC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGACUAUACCGGCAAUCGUGCAUCCCC 29
Claim 13; Fig 1A; 216pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.9%;
Best Local Similarity 72.4%;
Matches 21; Conservative
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Gaps

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GGGGACUAUACCGGCAAUCGUGCAUCCCC 29 GGGGACUAVACGUGAACGACUGCAUCCAC 29

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RESULT 11

Local Similarity

Matches

Mus sp.

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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                               17; leukocyte; gene expression profiling; allograft rejection;
atherosclerosis; congestive heart failure; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J; Ly N, Woodward R, Quertermous T, Johnson F;
                                                                                                                   Human leukocyte gene expression profiling probe SEQ ID NO 1519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.5%; Score 15.8; DB 6; Length 50; 63.0%; Pred. No. 8.7e+02; ative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50 BP; 8 A; 8 C; 15 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGACUAUACCGGCAAUCGUGCAUCCCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 374; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-2001; 2001WO-US047856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .911/c
ADA01911 standard; DNA; 105
                                                                  09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 63.0 es 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOC-) BIOCARDIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-636525/68.
                                                                                                                                                                                                                                                                                                                                         WO200257414-A2.
                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-2002.
                       ABZ01528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA01911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel murine cDNAs produced using gene trap technology. The OWNIRANK gene trapped sequences (GTSS) are individually identified novel genes, and are useful in functional genomic analysis, in the discovery and development of new therapeutic and disgnostic agents, for gene discovery, for diagnostic gene expression analysis, for cross species hybridisation analysis, and for genetic manipulations such as antisense inhibition or gene targeting. The polynucleotides of the invention are also useful for isolating cDNAs, genomic clones or full-length genes/polynucleotides, or their homologues, centerologues, paralogues or orthologues, that are capable of hybridising to one or more of the new murine polynucleotide sequences. The polynucleotides are also useful for identifying the coding regions of the murine genome, and as hybridisation probes. ABX90657-ABX91682 represent the murine GTSs of the invention. Noce: The sequence data for this patent coding to the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New murine polynucleotides comprising gene trapped sequences, useful in functional genomic analysis, in the development of new therapeutic or diagnostic agents, for diagnostic gene expression analysis or for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                            Murine; mouse; gene trap technology; gene trapped sequence; GTS; gene identification; functional genomic analysis; gene discovery; gene expression analysis; cross species hybridisation analysis; antisense inhibition; gene targeting; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 172 BP; 51 A; 53 C; 38 G; 26 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the USPTO web site at
                                                                                                                                                                                                                Murine gene trapped sequence (GTS) SEQ ID No 733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sands AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 733; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGACUAUACCGGCAAUCGUGCAUCC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/psipsDIDEntry.html
                                                                ABX91389 standard; cDNA; 172 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-2000; 2000US-00728444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0168360P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Friedrich G, Zambrowicz B,
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-288124/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FRIE/) FRIEDRICH G.
                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002161207-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      manipulations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1999;
                                                                                                                                                             07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2002
                                                                                                              ABX91389;
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Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; ds.
Mouse carcinoma associated nucleic acid, SEQ ID NO:430.
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ABZ01528/c ID ABZ01528 standard; DNA; 50 BP.

RESULT 13

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Gaps

26-DEC-2001; 2001WO-US051291.

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Search completed: April Job time: 105.035 secs
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                                                                                                                                                                                                                                                                                                       The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid a polypeptide (especially an antibody) that specifically hinds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protonnosquence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinoma (especially breast cancer, prostate cancer, lymphom or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The sequence of the invention. Note: The sequence data for unless caid also available in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma.
                                                                                                                                                                                                                                       recombinant nucleic acid encoding carcinoma associated protein, il for preparing compositions for treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.8; DB 8; Length 105;
Pred. No. 9.7e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 105 BP; 34 A; 21 C; 29 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse carcinoma associated gene fragment #430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%; Scor. 73.7%; Pred. No. 5...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                 Claim 1; Page 185; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGACUAUACCGGCAAUCG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || ||:||:|| |||||:||
27 GGTACTATACTGGCAATCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB71650 standard; DNA; 105 BP
                                                                                                26-DEC-2002; 2002WO-US041414
                                                                                                                           26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                      (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                             WPI; 2003-587068/55
                                       WO2003057146-A2.
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                                                                    17-JUL-2003
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                                                                                                                                                                                   Morris DW;
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                Mus sp.
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The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The sequences shown in ADB71221-ADB72172 represent mouse sequence tags, or genomic insertion sites, of carcinoma associated (CA) genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 105 BP; 34 A; 21 C; 29 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 144; 2304pp; English.
02-MAR-2001, 2001US-00798586.
23-CCT-2001, 2001US-00004113.
08-NOV-2001, 2001US-0055482.
30-NOV-2001, 2001US-00937722.
20-DEC-2001, 2001US-00034650.
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Best Local Similarity 73.73
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                   Engelhard EK;
                                                                                                                                                                                                                                (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-239337/23.
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